



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 114657

TO: Rita Mitra
Location: rem/3b65
Art Unit: 1653
Thursday, February 19, 2004

Case Serial Number: 09/786260

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen E01A69
Phone: 571-272-2518 *BOB*

barbara.obryen@uspto.gov

Search Notes

oligo search

O'Bryen, Barbara

From: Mitra, Rita
Sent: Thursday, February 19, 2004 2:43 PM
To: O'Bryen, Barbara
Subject: RE: serach ready

Barbara

Thanks a lot.

I see that in database A_Geneseq_19Jun03, there are 30 hits with 100% homology. Could you please print them all (hit no. beyond 15) for me?

Rita

-----Original Message-----

From: O'Bryen, Barbara
Sent: Thursday, February 19, 2004 10:20 AM
To: Mitra, Rita
Subject: serach ready

You can pick it up at the Information Desk in the library.

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

protein - protein search, using sw model

on: February 18, 2004, 14:39:00 ; Search time 41 Seconds
(without alignments)
460.694 Million cell updates/sec

le: US-09-786-260-1
fect score: 119
gence: 1 MKVLISLLILLPLMLSMV.....SRACQFLKQCQLRSFALPL 119

ring table: OLIGO
Gapop 60.0 , Gapext 60.0

rched: 1107863 seqs, 158726573 residues

d size : 0
al number of hits satisfying chosen parameters: 1107863

imum DB seq length: 0
imum DB seq length: 2000000000

t-processing: Listing first 45 summaries

abase : A.Geneseq.19Jun03.*
1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match	Length	DB ID	Description
1	119	100.0	119	21	Human secreted pro
2	119	100.0	119	21	Human TGC-440 secr
3	119	100.0	119	21	Human signal pepti
4	119	100.0	119	21	Membrane-bound pro
5	119	100.0	119	22	Human PRO polypept
6	119	100.0	119	22	Amino acid sequenc
7	119	100.0	119	22	Human PRO842. Hom
8	119	100.0	119	22	Human PRO842. UNQ4
9	119	100.0	119	23	Human cytokine PRO

10	119	100.0	119	23	ABG95863	Human secreted/tra
11	119	100.0	119	24	ABU71181	Human PRO842 prote
12	119	100.0	119	24	ABU71518	Human secreted pol
13	119	100.0	119	24	ABU71964	Novel human secret
14	119	100.0	119	24	ABU72121	Human PRO polypept
15	119	100.0	119	24	ABU65638	Human secreted/tra
16	119	100.0	119	24	ABU65971	Novel human secret
17	119	100.0	119	24	ABU67475	Human secreted/tra
18	119	100.0	119	24	ABU65333	Human PRO polypept
19	119	100.0	119	24	ABU59084	Novel human secret
20	119	100.0	119	24	ABU59231	Human secreted/tra
21	119	100.0	119	24	ABU59380	Novel human secret
22	119	100.0	119	24	ABU60515	Human secreted/tra
23	119	100.0	119	24	ABU58006	Human PRO polypept
24	119	100.0	119	24	ABU58469	Human PRO polypept
25	119	100.0	119	24	ABU58937	Human secreted/tra
26	119	100.0	119	24	ABU56005	Human secreted/tra
27	119	100.0	119	24	ABU57000	Human PRO polypept
28	119	100.0	119	24	ABU13897	Human PRO842 polyp
29	119	100.0	119	24	ABU10579	Human secreted/tra
30	119	100.0	119	24	ABU10852	Human PRO polypept
31	97	81.5	97	21	AA182454	Mature human TGC-4
32	93	78.2	93	19	AAW83953	Polypeptide encode
33	69	58.0	69	20	AAV11732	Human 5' EST secre
34	37	31.1	64	19	AAW83938	Human secreted pro
35	24	20.2	48	20	AAV11731	Human 5' EST secre
36	13	10.9	97	21	AAV82458	Mature mouse TGC-4
37	13	10.9	119	21	AAV82457	Mouse TGC-440 secr
38	9	7.6	144	21	AAW09686	Arabidopsis thalia
39	8	6.7	58	22	AAU22441	Human cardiovascu
40	8	6.7	60	22	ABG57426	Human liver peptid
41	8	6.7	60	22	ABE41994	Peptide #9500 enco
42	8	6.7	60	22	ABE25625	Protein #7624 enco
43	8	6.7	60	22	AAW62872	Human brain expres
44	8	6.7	60	22	AAW75685	Human bone marrow
45	8	6.7	60	22	AAW35795	Peptide #9832 enco

ALIGNMENTS

RESULT 1
AAB34728
ID AAB34728 standard; Protein; 119 AA.
XX AAB34728;
AC AAB34728;
DT 26-JAN-2001 (first entry)
XX Human secreted protein encoded by DNA clone vq8 1.
DE Human secreted protein encoded by DNA clone vq8 1.
XX Secreted protein; human; autoimmune disorder; multiple sclerosis; ulcer;
KW systemic lupus erythematosus; rheumatoid arthritis; anaemia; stroke;
KW haematopoiesis regulation; tissue regrowth; wound healing; haemophilia;
KW Alzheimer's disease; Parkinson's disease; Shy-drager syndrome; cancer;
KW contraceptive; infection; growth inhibition; hyperproliferative disorder;
KW psoriasis.
XX Homo sapiens.
XX WO200055375-A1.
PN 21-SEP-2000.
PD 17-MAR-2000; 2000WO-US07285.
XX 17-MAR-1999; 99US-0124808.
PR 17-MAR-1999; 99US-0124916.
PR 17-AUG-1999; 99US-0149639.
PR 01-OCT-1999; 99US-0157247.
PR 29-NOV-1999; 99US-0167824.
PR 15-FEB-2000; 2000US-0182711.
XX

(ALPH-) ALPHAGENE INC.

Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;

WPI; 2000-638211/61.

N-PSDB; AAC59829.

Novel proteins and polypeptides useful for the treatment of e.g. multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, cancer, Alzheimer's disease, Parkinson's disease, stroke, anemia and ulcers -

Claim 92; Page 441-442; 493pp; English.

This invention relates to 59 human secreted proteins and the nucleotide sequences encoding them. Sequences AAC59788-C59846 and AAB34687-B34745 represent the proteins and their encoding nucleotide sequences, and sequences AAB34746-B34771 represent fragments of the proteins. Probes for the DNA sequences are represented by sequences AAC59847-C59596. The proteins exhibit neuroprotective, dermatological, immunosuppressive, antiinflammatory, antianaemic, nootropic, antiparkinsonian, cerebroprotective, haemostatic, vulnetary, cytostatic, antipsoriatic, antibacterial, virucide, and fungicide activity. The proteins and nucleotide sequences are useful as nutritional sources or supplements and in research. The proteins are useful for treating immune deficiency and disorders, which may be genetic or resulting from infections, autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, and for treating myeloid or lymphoid cell deficiencies such as anaemias by regulating haematopoiesis. The proteins are also useful in compositions for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, for wound healing, tissue repair and replacement and in the treatment of wounds, incisions and ulcers. Other uses include in the treatment of central and peripheral nervous system and neuropathies such as Alzheimer's and Parkinson's diseases and Shy-Drager syndrome, and mechanical and traumatic disorders, such as spinal cord disorders, head trauma and strokes. The proteins may also be used as a contraceptive, and for treating coagulation disorders such as haemophilias. The protein and nucleotide sequences with cadherin activity are useful for treating cancer. Other uses for the protein include for inhibiting the growth, infection or function of, or killing, infectious agents such as bacteria, virus, fungi and other parasites, for effecting bodily characteristics such as height, weight, hair colour, effecting biorhythms or cardiac cycles or rhythms, effecting metabolism, catabolism, anabolism, lipid processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors, effecting behavioural characteristics, providing analgesic effects and for treating hyperproliferative disorders such as psoriasis.

Sequence 119 AA;

Query Match 100.0%; Score 119; DB 21; Length 119;

Best Local Similarity 100.0%; Pred. No. 3.3e-110;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVLISLLLLPLMLSMVSSSLNPGVARGHRDQASRRWLQGGQCECKDWFRLAP 60

1 MKVLISLLLLPLMLSMVSSSLNPGVARGHRDQASRRWLQGGQCECKDWFRLAP 60

61 RRKFTVSGLPKQPCDHFPGKGNVKKTRHQRHRRKPNKHSRACQFLKQCQLRSFALPL 119

61 RRKFTVSGLPKQPCDHFPGKGNVKKTRHQRHRRKPNKHSRACQFLKQCQLRSFALPL 119

SULT 2
Y82453

AA182453 standard; Protein; 119 AA.

AA182453;

30-JUN-2000 (first entry)

Human TGC-440 secretory protein SEQ ID NO:1.

XX TGC-440; secretory protein; immunological disease; infectious disease;
KW pulmonary function disorder; hepatic function disorder; nephrotropic;
KW gastrointestinal function disorder; antiinflammatory; immunomodulatory;
KW virucide; hepatotropic; antiasthmatic; antibacterial; vaccine;
KW hepatitis; nephritis; influenza; asthma; pulmonary hypertension;
KW pneumonia; Helicobacter pylori infection.

OS Homo sapiens.

XX WO200014226-A1.

XX 16-MAR-2000.

XX 02-SEP-1999; 99WO-JP04765.

XX 03-SEP-1998; 98JP-0250108.

XX (TAKE) TAKEDA CHEM IND LTD.

PI Itoh Y, Ogi K, Tanaka H, Kitada C;

XX WPI; 2000-356978/22.

DR N-PSDB; AAA08343, AAA08344.

XX Secretory protein TGC440, antibodies to it and compounds promoting or
PT inhibiting its activity for diagnosis and treatment of diseases of the
PT immune system, lung, kidney, liver and intestinal system -

XX Claim 1; Fig 1; 86pp; Japanese.

XX The present sequence represents a human secretory protein designated
CC TGC-440. TGC-440 has antiinflammatory, nephrotropic, immunomodulatory,
CC virucide, hepatotropic, antiasthmatic and antibacterial activities,
CC and can be used in vaccines. TGC-440 and the polynucleotide sequence
CC encoding it can be used to treat, prevent and diagnose immunological,
CC lung, liver, kidney or gastrointestinal disorders and infectious
CC diseases, such as hepatitis, nephritis, influenza, asthma, pneumonia,
CC pulmonary hypertension, and Helicobacter pylori infection. An antibody
CC immunospecific for TGC-440 is also useful in the above treatment and
CC diagnosis, and also for quantifying the amount of TGC-440 in a liquid
CC specimen.

XX Sequence 119 AA;

Query Match 100.0%; Score 119; DB 21; Length 119;

Best Local Similarity 100.0%; Pred. No. 3.3e-110;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLISLLLLPLMLSMVSSSLNPGVARGHRDQASRRWLQGGQCECKDWFRLAP 60

Db 1 MKVLISLLLLPLMLSMVSSSLNPGVARGHRDQASRRWLQGGQCECKDWFRLAP 60

QY 61 RRKFTVSGLPKQPCDHFPGKGNVKKTRHQRHRRKPNKHSRACQFLKQCQLRSFALPL 119

Db 61 RRKFTVSGLPKQPCDHFPGKGNVKKTRHQRHRRKPNKHSRACQFLKQCQLRSFALPL 119

RESULT 3

AA182453

ID AA182453 standard; Protein; 119 AA.

XX AA182453;

XX 11-MAY-2000 (first entry)

XX Human signal peptide containing protein HSPP-94 SEQ ID NO:94.

Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
KW antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
KW reproductive disorder; developmental disorder; arteriosclerosis;

cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; Parkinson's disease; Huntington's diseases; ovulatory defect; muscular dystrophy.

Homo sapiens.

W020000610-A2.

06-JAN-2000.

25-JUN-1999; 99WO-US14484.

26-JUN-1998; 98US-0090762.

31-JUL-1998; 98US-0094983.

01-OCT-1998; 98US-0102686.

11-DEC-1998; 98US-0112129.

(INCY-) INCYTE PHARM INC.

Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR; Akerbloom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL; Bandman O;

WPI: 2000-160673/14.

N-PSDB; AAZ98202.

New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease

Claim 1; Page 220-221; 327pp; English.

AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic, neuroprotective, cardiovascular and antiasthmatic activities, and can be used in gene therapy. HSPPs can be used to treat or prevent disorders associated with decreased activity or function of HSPP. Antagonists of HSPP are used to treat or prevent disorders associated with increased activity or function of HSPP. Such diseases include cell proliferation (including cancer), inflammation, cardiovascular, neurological, reproductive or developmental disorders, (e.g. arteriosclerosis, cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia, asthma, Crohn's disease, microbial or other infections, congestive or ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP nucleic acids can be used for the recombinant production of HSPP, for detecting HSPP in standard hybridisation and amplification assays (for diagnosis and monitoring), in gene therapy, as antisense, triplex-forming or ribozyme therapeutics, for detecting related sequences or genetic variations, and for chromosomal mapping. HSPP are also used to raise specific antibodies (Ab) and to screen for agonists and antagonists (potential therapeutic agents). Ab are used to diagnose, or monitor, HSPP-related diseases (in usual immunoassays), as therapeutic antagonists, in competitive drug screens, and for purification of HSPP from natural sources.

Sequence 119 AA;

very Match 100.0%; Score 119, DB 21; Length 119;
est Local Similarity 100.0%; Pred. NO. 3.3e-110; Mismatches 0; Gaps 0;
atches 119; Conservative 0; Indels 0;

1 MKVLISLLLLLPLMLMSVSSSLNPGVARGHSDRGQASRRWLQEGGQCECKDWFLRAP 60

1 MKVLISLLLLLPLMLMSVSSSLNPGVARGHSDRGQASRRWLQEGGQCECKDWFLRAP 60

61 RRKMTVSGLPKQCPDCHFKGNVYKTKTHORHHRKPNKHSRACQQLKQCLRSFALPL 119

61 RRKMTVSGLPKQCPDCHFKGNVYKTKTHORHHRKPNKHSRACQQLKQCLRSFALPL 119

RESULT 4

AAZ98202

ID AAY66668 standard; protein; 119 AA.

XX AAY66668;

AC AAY66668;

XX 05-APR-2000 (first entry)

DT 05-APR-2000 (first entry)

XX Membrane-bound protein PRO842.

DE Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;

KW pharmaceutical; receptor immunoadhesin; gene mapping.

KW pharmaceutical; receptor immunoadhesin; gene mapping.

XX Homo sapiens.

OS WO9963088-A2.

XX 09-DEC-1999.

PD 09-DEC-1999.

XX 02-JUN-1999; 99WO-US12252.

PF 02-JUN-1998; 98US-0087607.

XX 02-JUN-1998; 98US-0087609.

PR 02-JUN-1998; 98US-0087759.

PR 03-JUN-1998; 98US-0087827.

PR 04-JUN-1998; 98US-0088021.

PR 04-JUN-1998; 98US-0088025.

PR 04-JUN-1998; 98US-0088028.

PR 04-JUN-1998; 98US-0088029.

PR 04-JUN-1998; 98US-0088030.

PR 04-JUN-1998; 98US-0088033.

PR 04-JUN-1998; 98US-0088326.

PR 05-JUN-1998; 98US-0088167.

PR 05-JUN-1998; 98US-0088202.

PR 05-JUN-1998; 98US-0088212.

PR 05-JUN-1998; 98US-0088217.

PR 09-JUN-1998; 98US-0088655.

PR 10-JUN-1998; 98US-0088722.

PR 10-JUN-1998; 98US-0088730.

PR 10-JUN-1998; 98US-0088734.

PR 10-JUN-1998; 98US-0088738.

PR 10-JUN-1998; 98US-0088740.

PR 10-JUN-1998; 98US-0088741.

PR 10-JUN-1998; 98US-0088742.

PR 10-JUN-1998; 98US-0088810.

PR 10-JUN-1998; 98US-0088811.

PR 10-JUN-1998; 98US-0088824.

PR 10-JUN-1998; 98US-0088825.

PR 10-JUN-1998; 98US-0088826.

PR 11-JUN-1998; 98US-0088858.

PR 11-JUN-1998; 98US-0088861.

PR 11-JUN-1998; 98US-0088863.

PR 11-JUN-1998; 98US-0088876.

PR 12-JUN-1998; 98US-0089090.

PR 12-JUN-1998; 98US-0089105.

PR 16-JUN-1998; 98US-0089440.

PR 16-JUN-1998; 98US-0089512.

PR 16-JUN-1998; 98US-0089514.

PR 17-JUN-1998; 98US-0089532.

PR 17-JUN-1998; 98US-0089538.

PR 17-JUN-1998; 98US-0089598.

PR 17-JUN-1998; 98US-0089600.

PR 17-JUN-1998; 98US-0089653.

PR 18-JUN-1998; 98US-0089801.

PR 18-JUN-1998; 98US-0089907.

PR 18-JUN-1998; 98US-0089908.

PR 19-JUN-1998; 98US-0089947.

PR 19-JUN-1998; 98US-0089948.

PR 19-JUN-1998; 98US-0089952.

PR 22-JUN-1998; 98US-0090246.

PR 22-JUN-1998; 98US-0090252.

PR 22-JUN-1998; 98US-0090254.

23-JUN-1998; 98US-0090349.
 23-JUN-1998; 98US-0090355.
 24-JUN-1998; 98US-0090429.
 24-JUN-1998; 98US-0090431.
 24-JUN-1998; 98US-0090435.
 24-JUN-1998; 98US-0090444.
 24-JUN-1998; 98US-0090445.
 24-JUN-1998; 98US-0090461.
 24-JUN-1998; 98US-0090472.
 24-JUN-1998; 98US-0090535.
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 24-JUN-1998; 98US-0090557.
 25-JUN-1998; 98US-0090676.
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 25-JUN-1998; 98US-0090688.
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 25-JUN-1998; 98US-0090691.
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 25-JUN-1998; 98US-0090696.
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 01-JUL-1998; 98US-0091358.
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 02-JUL-1998; 98US-0091628.
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 02-JUL-1998; 98US-0091673.
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 07-JUL-1998; 98US-0091982.
 08-JUL-1998; 98US-0092182.
 10-JUL-1998; 98US-0092472.
 20-JUL-1998; 98US-0093339.
 30-JUL-1998; 98US-0094651.
 04-AUG-1998; 98US-0095282.
 04-AUG-1998; 98US-0095285.
 04-AUG-1998; 98US-0095301.
 04-AUG-1998; 98US-0095302.
 04-AUG-1998; 98US-0095318.
 04-AUG-1998; 98US-0095321.
 04-AUG-1998; 98US-0095325.
 10-AUG-1998; 98US-0095916.
 10-AUG-1998; 98US-0095929.
 10-AUG-1998; 98US-0096012.
 11-AUG-1998; 98US-0096143.
 11-AUG-1998; 98US-0096146.
 12-AUG-1998; 98US-0096329.
 17-AUG-1998; 98US-0096757.
 17-AUG-1998; 98US-0096766.
 17-AUG-1998; 98US-0096768.
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 17-AUG-1998; 98US-0096894.
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 18-AUG-1998; 98US-0097022.
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26-AUG-1998; 98US-0097954.
 26-AUG-1998; 98US-0097955.
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 26-AUG-1998; 98US-0097979.
 26-AUG-1998; 98US-0097986.
 26-AUG-1998; 98US-0098014.
 31-AUG-1998; 98US-0098525.
 16-SEP-1998; 98US-0100634.
 12-JAN-1999; 99US-0115565.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
 PI Wood WI, Yuan J;
 XX
 DR WPI; 2000-072883/06.
 DR N-PSDB; AAZ65001.
 XX
 PT Membrane-bound proteins and related nucleotide sequences -
 XX
 PS claim 12; Fig 99; 822pp; English.
 XX
 CC The invention provides membrane-bound PRO polypeptides and
 CC polynucleotides encoding them. The PRO sequences of the invention were
 CC identified based on extracellular domain homology screening. The PRO
 CC sequences have homology with proteins including LDL receptors, TIE
 CC ligands and various enzymes. The membrane-bound proteins and receptor
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
 CC immunoadhesins, for instance, can be used as therapeutic agents to block
 CC receptor-ligand interactions. The membrane-bound proteins can also be
 CC employed for screening of potential peptide or small molecule inhibitors
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences
 CC are useful as hybridization probes, in chromosome and gene mapping and in
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
 CC will also be useful for the preparation of PRO polypeptides, especially
 CC by recombinant techniques.
 XX
 SQ Sequence 119 AA;
 Query Match 100.0%; Score 119; DB 21; Length 119;
 Best Local Similarity 100.0%; Pred. No. 3.3e-110;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKVLISLLLLLLPLMLMSVSSSLNPGVARGHRDGOASRRWLQEGQCECKDWFLRAP 60
 Db 1 MKVLISLLLLLLPLMLMSVSSSLNPGVARGHRDGOASRRWLQEGQCECKDWFLRAP 60
 QY 61 RKFKMTVSGLPKQPCDHFKNVYKTRHQRHKKPNKHSRACQQLKQQLRSFALPL 119
 Db 61 RKFKMTVSGLPKQPCDHFKNVYKTRHQRHKKPNKHSRACQQLKQQLRSFALPL 119
 RESULT 5
 AAU29093
 ID AAU29093 standard; Protein; 119 AA.
 XX
 AC AAU29093;
 XX
 DT 19-DEC-2001 (first entry)
 XX
 DE Human PRO polypeptide sequence #70.
 XX
 KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200168848-A2.
 XX

20-SEP-2001.

28-FEB-2001; 2001WO-US06520.

01-MAR-2000; 2000WO-US05601.
02-MAR-2000; 2000WO-US05841.
03-MAR-2000; 2000US-187202P.
06-MAR-2000; 2000US-186968P.
14-MAR-2000; 2000US-189320P.
14-MAR-2000; 2000US-189328P.
15-MAR-2000; 2000WO-US06884.
21-MAR-2000; 2000US-190828P.
21-MAR-2000; 2000US-191007P.
21-MAR-2000; 2000US-191048P.
21-MAR-2000; 2000US-191314P.
28-MAR-2000; 2000US-192655P.
29-MAR-2000; 2000US-193032P.
29-MAR-2000; 2000US-193053P.
30-MAR-2000; 2000WO-US08439.
04-APR-2000; 2000US-194443P.
04-APR-2000; 2000US-194647P.
11-APR-2000; 2000US-195975P.
11-APR-2000; 2000US-196000P.
11-APR-2000; 2000US-196187P.
11-APR-2000; 2000US-196690P.
11-APR-2000; 2000US-196820P.
18-APR-2000; 2000US-198121P.
18-APR-2000; 2000US-198585P.
25-APR-2000; 2000US-199397P.
25-APR-2000; 2000US-199550P.
25-APR-2000; 2000US-199654P.
03-MAY-2000; 2000US-201516P.
17-MAY-2000; 2000WO-US13705.
22-MAY-2000; 2000WO-US14042.
30-MAY-2000; 2000WO-US14941.
02-JUN-2000; 2000WO-US15284.
05-JUN-2000; 2000US-209832P.
28-JUL-2000; 2000WO-US20710.
22-AUG-2000; 2000US-0644848.
24-AUG-2000; 2000WO-US23328.
08-NOV-2000; 2000WO-US30952.
01-DEC-2000; 2000WO-US32678.
20-DEC-2000; 2000WO-US34956.

(GETH) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

WPI; 2001-602746/68.
N-PSDB; AAS45994.

Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals and to screen for modulators of the compounds -

Claim 11; Fig 140; 774pp; English.

Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention. The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids

CC can be used for genetic analysis of individuals with genetic disorders.

XX SQ Sequence 119 AA;

Query Match 100.0%; Score 119; DB 22; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-110;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFLRAP 60

DB 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFLRAP 60

QY 61 RRKFMTVSGLPKFKQPCDHFKGNVKTQRHRRKPKHSRACQOFLKQCQLRSFALPL 119

DB 61 RRKFMTVSGLPKFKQPCDHFKGNVKTQRHRRKPKHSRACQOFLKQCQLRSFALPL 119

RESULT 6

RAG63977
ID AAG63977 standard; Protein; 119 AA.

XX AC AAG63977;

XX DT 13-NOV-2001 (first entry)

XX DE Amino acid sequence of a human Lngl04 polypeptide.

XX KW Human; lung cancer specific gene; LSG; Lngl04; lung cancer.

XX OS Homo sapiens.

XX PN WO200161055-A2.

XX PD 23-AUG-2001.

XX PF 20-FEB-2001; 2001WO-US05674.

XX PR 17-FEB-2000; 2000US-0183188.

XX PA (DIAD-) DIADEXUS INC.

XX FI Chen S, Sun Y, Macina RA;

XX DR WPI; 2001-529917/58.

XX DR N-PSDB; AAH77949, AAH77951.

XX PT New lung cancer specific gene for the treatment and diagnosis of lung cancer -

XX PS Claim 2; Page 115-116; 119pp; English.

XX CC The present sequence is encoded by a human lung cancer specific gene (LSG), and represents a polypeptide designated Lngl04. LSGs are useful in the treatment and diagnosis of lung cancer. The treatment of lung cancer comprises the administration of a molecule which down regulates the expression of an LSG. An immune response can be mounted against a target cell expressing an LSG. Identification of potential therapeutic agents for use in imaging and treating lung cancer which comprises screening molecules for an ability to bind to or decrease expression of an LSG relative to LSG in the absence of the agent where the ability of a molecule to bind to the LSG or decrease expression of the LSG is indicative of the molecule being useful in imaging and treating lung cancer.

XX SQ Sequence 119 AA;

Query Match 100.0%; Score 119; DB 22; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-110;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFLRAP 60

DB 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFLRAP 60

61 RRKFTVTVGLPKKQPCDHFHKGKGVKTRHQRHHRKPNKHSRACQOFLKQCQLRSFALPL 119
 61 RRKFTVTVGLPKKQPCDHFHKGKGVKTRHQRHHRKPNKHSRACQOFLKQCQLRSFALPL 119

ULT 7
 387538
 AAB87538 standard; Protein; 119 AA.

AAB87538;

15-MAY-2001 (first entry)

Human PRO842.

Human; PRO protein; mapping.

Homo sapiens.

WO200116318-A2.

08-MAR-2001.

24-AUG-2000; 2000WO-US23328.

01-SEP-1999; 99WO-US20111.
 15-SEP-1999; 99WO-US21090.
 07-DEC-1999; 99US-0169495.
 09-DEC-1999; 99US-0170262.
 11-JAN-2000; 2000US-0175481.
 18-FEB-2000; 2000WO-US04341.
 18-FEB-2000; 2000WO-US04342.
 22-FEB-2000; 2000WO-US04414.
 01-MAR-2000; 2000WO-US05601.
 03-MAR-2000; 2000US-0187202.
 25-APR-2000; 2000US-0199397.
 22-MAY-2000; 2000WO-US14042.
 05-JUN-2000; 2000US-0209832.

(GETH) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;

WPI; 2001-183260/18.
 N-PSDB; AAF92070.

Eighty four nucleic acids encoding PRO polypeptides, useful in
 molecular biology, including use as hybridization probes, and in
 chromosome and gene mapping.

Claim 12; Fig 26; 278pp; English.

The present sequence is a human PRO polypeptide (secreted and
 transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
 anti-PRO antibodies are useful for preparation of a medicament useful in
 the treatment of a condition which is responsive to the PRO protein,
 agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
 employed as molecular weight markers for protein electrophoresis. The PRO
 coding sequence has applications in molecular biology, including use as
 hybridisation probes, and in chromosome and gene mapping.

Sequence 119 AA;

Query Match 100.0%; Score 119; DB 22; Length 119;
 Best Local Similarity 100.0%; Pred. No. 3.3e-110; Indels 0; Gaps 0;
 Matches 119; Conservative 0; Mismatches 0;

1 MKVLISLLILLPLMLMSVSSINFGVARGHRDRGQASRRWLQGGQCECKDWFLRAP 60
 1 MKVLISLLILLPLMLMSVSSINFGVARGHRDRGQASRRWLQGGQCECKDWFLRAP 60

OY 61 RRKFTVTVGLPKKQPCDHFHKGKGVKTRHQRHHRKPNKHSRACQOFLKQCQLRSFALPL 119
 DB 61 RRKFTVTVGLPKKQPCDHFHKGKGVKTRHQRHHRKPNKHSRACQOFLKQCQLRSFALPL 119

RESULT 8

AAB65191

ID AAB65191 standard; Protein; 119 AA.

XX AC AAB65191;

XX 02-APR-2001 (first entry)

XX Human PRO842 (UNQ473) protein sequence SEQ ID NO:165.

XX Human; secreted and transmembrane protein; PRO; cytostatic;
 KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
 KW diagnostic assay.

XX Homo sapiens.

XX WO2000073454-A1.

XX 07-DEC-2000.

XX 30-MAR-2000; 2000WO-US08439.

XX 02-JUN-1999; 99WO-US12252.
 XX 23-JUN-1999; 99US-0141037.
 XX 07-JUL-1999; 99US-0143048.
 XX 20-JUL-1999; 99US-0144758.
 XX 26-JUL-1999; 99US-0145698.
 XX 28-JUL-1999; 99US-0146222.
 XX 17-AUG-1999; 99US-0149396.
 XX 15-SEP-1999; 99WO-US21090.
 XX 15-SEP-1999; 99WO-US21547.
 XX 08-OCT-1999; 99US-0159663.
 XX 30-NOV-1999; 99WO-US28313.
 XX 01-DEC-1999; 99WO-US28301.
 XX 16-DEC-1999; 99WO-US30095.
 XX 20-DEC-1999; 99WO-US30911.
 XX 05-JAN-2000; 2000WO-US00219.
 XX 06-JAN-2000; 2000WO-US00376.
 XX 11-FEB-2000; 2000WO-US03565.
 XX 18-FEB-2000; 2000WO-US04341.
 XX 22-FEB-2000; 2000WO-US04414.
 XX 24-FEB-2000; 2000WO-US04914.
 XX 24-FEB-2000; 2000WO-US05004.
 XX 02-MAR-2000; 2000WO-US05841.
 XX 15-MAR-2000; 2000WO-US06884.
 XX 20-MAR-2000; 2000WO-US07377.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 XX Zhang Z;

XX WPI; 2001-032160/04.
 XX N-PSDB; AAF44147.

XX PRO polynucleotides used to produce polypeptides used to target
 PT bioactive molecules such as toxins, radiolabels or antibodies, to
 PT specific cells, to cause targeted cell death -

XX Claim 12; Fig 99; 935pp; English.

XX The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
 CC can be used for targeted delivery of bioactive molecules, such as
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide

sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF44470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to AAB65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.

Sequence 119 AA;

Query March 100.0%; Score 119; DB 22; Length 119;
 Best Local Similarity 100.0%; Pred. No. 3.3e-110;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFLRAP 60
 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFLRAP 60
 61 RRKPMVTSGLPKKQCCDHFKNVKTTRHQRHRRKPKNHSRACQQLKQQLRSFALPL 119
 61 RRKPMVTSGLPKKQCCDHFKNVKTTRHQRHRRKPKNHSRACQQLKQQLRSFALPL 119

JLT 9

54931

ABP54931 standard; Protein; 119 AA.

ABP54931;

08-JAN-2003 (first entry)

Human cytokine PRO842 (CK27).

PRO842; CK27; chemokine; human; antiinflammatory; dermatological;
 hepatotropic; anti-allergic; antiasthmatic; immunosuppressive;
 antithyroid; antidiabetic; antianaemic; haemostatic; antipsoriatic;
 antirheumatic; antiarthritic; nephrotropic.

Homo sapiens.

Key	Location/Qualifiers
Peptide	1..22
Protein	/label= Signal_peptide 23..119
Modified-site	/label= Mature_protein 27..32
Modified-site	/note= "potential N-myristoylation site"
Modified-site	/note= "potential protein kinase C phosphorylation site"
Modified-site	/note= "potential N-myristoylation site"

WO200270706-A2.

12-SEP-2002.

07-DEC-2001; 2001WO-US48060.

28-FEB-2001; 2001WO-US06520.

28-AUG-2001; 2001US-0941992.

(GETH) GENENTECH INC.

French D, Grimaldi JC, Hilian KJ, Pisabarro MT, Schmidt KN,
 Smith V, Tumas D, Vandlen RL, Watanabe CK, Williams PM, Wood WT;

WPI: 2002-750461/81.

N-PSDB; ABV73914.

PT New PRO842 polypeptides having structural homology to interleukin-8,
 PT useful for treating or diagnosing a mammal with an inflammatory disease
 PT or immune related disease, e.g. rheumatoid arthritis, osteoarthritis or
 PT allergic disease .

XX Claim 1; Fig 2; 118pp; English.

XX The present sequence is the protein sequence of PRO842 (CK27),
 CC a novel human chemokine (mol.wt. 13.8 kDa, pI 11.16) having
 CC structural homology to interleukin-8. Microarray analysis has
 CC shown PRO842 to be over-expressed in colon tumour, lung tumour and
 CC breast tumour cells compared with non-cancerous human tissue,
 CC making it a useful diagnostic marker for cancerous tumours and a
 CC therapeutic target. PRO842 also plays a role in the inflammatory
 CC response, having chemotactic properties toward monocytes and
 CC dendritic cells. The invention provides PRO842 polypeptides,
 CC polynucleotides, host cells, vectors and antibodies, as well as
 CC methods of treating an immune related disorder by using a PRO842
 CC polypeptide, or an agonist, antagonist or antibody. The immune
 CC related disorder may be systemic lupus erythematosus, rheumatoid
 CC arthritis, osteoarthritis, juvenile chronic arthritis,
 CC spondyloarthritis, systemic sclerosis, idiopathic inflammatory
 CC myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis,
 CC autoimmune haemolytic anaemia, autoimmune thrombocytopaenia,
 CC thyroiditis, diabetes mellitus, immune-mediated renal disease,
 CC demyelinating disease of the central or peripheral nervous system,
 CC idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC chronic inflammatory demyelinating polyneuropathy, hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous
 CC skin disease, erythema multiforme, contact dermatitis, psoriasis,
 CC an allergic disease, asthma, allergic rhinitis, atopic dermatitis,
 CC food hypersensitivity, urticaria, an immunologic disease of the
 CC ovaries, an immunologic disease of the lung, eosinophilic
 CC pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection
 CC or graft-versus-host-disease (all claimed).

Sequence 119 AA;

Query Match 100.0%; Score 119; DB 23; Length 119;
 Best Local Similarity 100.0%; Pred. No. 3.3e-110; Indels 0; Gaps 0;
 Matches 119; Conservative 0; Mismatches 0;

QY 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFLRAP 60
 DB 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFLRAP 60
 QY 61 RRKPMVTSGLPKKQCCDHFKNVKTTRHQRHRRKPKNHSRACQQLKQQLRSFALPL 119
 DB 61 RRKPMVTSGLPKKQCCDHFKNVKTTRHQRHRRKPKNHSRACQQLKQQLRSFALPL 119

RESULT 10

ABG95863

ID ABG95863 standard; Protein; 119 AA.

XX ABG95863;

10-DEC-2002 (first entry)

Human secreted/transmembrane protein PRO842.

XX Human; secreted protein; transmembrane protein; antirheumatic;
 KW antiarthritic; osteopathic; sports-related joint problem;
 KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.

XX Homo sapiens.

US2002119130-A1.

XX

29-AUG-2002.

06-DEC-2001; 2001US-0006967.

29-OCT-1997; 97US-063435P.

29-OCT-1997; 97US-064215P.

22-APR-1998; 98US-082797P.

29-APR-1998; 98US-083495P.

15-MAY-1998; 98US-085579P.

10-JUN-1998; 98US-088811P.

10-JUN-1998; 98US-088824P.

10-JUN-1998; 98US-088863P.

12-JUN-1998; 98US-089105P.

16-JUN-1998; 98US-089514P.

16-SEP-1998; 98WO-US19330.

08-MAR-1999; 99WO-US05028.

14-MAY-1999; 99WO-US10733.

02-JUN-1999; 99WO-US12252.

01-SEP-1999; 99WO-US20111.

15-SEP-1999; 99WO-US21090.

15-SEP-1999; 99WO-US21194.

22-DEC-1999; 99WO-US30720.

18-FEB-2000; 2000WO-US04341.

19-FEB-2000; 2000WO-US04342.

30-MAR-2000; 2000WO-US08439.

22-MAY-2000; 2000WO-US14042.

02-JUN-2000; 2000WO-US15264.

23-AUG-2000; 2000WO-US23522.

24-AUG-2000; 2000WO-US23328.

10-NOV-2000; 2000WO-US30873.

01-DEC-2000; 2000WO-US32378.

20-DEC-2000; 2000WO-US34956.

28-FEB-2001; 2001WO-US06520.

20-JUN-2001; 2001WO-US19692.

29-JUN-2001; 2001WO-US21066.

09-JUL-2001; 2001WO-US21735.

(GETH) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PU,

Grimaldi JC, Gurney AL, Watanabe CK, Wood WI,

WPI; 2002-731348/79.

N-PSDB; ABS74390.

New isolated secreted and transmembrane PRO polypeptide useful for modulating biological activity of a cell, or for treating sports-related joint problems, osteoarthritis or rheumatoid arthritis

Claim 20; Fig 26; 399pp; English.

The invention relates to an isolated secreted and transmembrane PRO polypeptide having 80 % sequence identity to a sequence appearing as AEG95951-ABG95934 or their associated signal peptide, or a sequence of an extracellular domain of the proteins with their associated signal peptide or lacking its associated signal peptide. Also included are the nucleic acids encoding the proteins, vectors, host cells, fusion proteins and antibodies which specifically bind to the proteins. The proteins are useful for detecting a polypeptide designated as A, B, C or D in a sample suspected of containing an A, B, C or D polypeptide, by contacting the sample with a polypeptide designated as E, F, G, H or I (or vice versa) and determining the formation of a A/E, B/F, C/H or D/I polypeptide conjugate in the sample, where the formation of the conjugate is indicative of the presence of an A, B, C or D polypeptide in the sample, where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801 polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G, H or I polypeptide is labeled with a detectable label or is attached to a solid support. The proteins are useful for linking a bioactive molecule to a cell expressing a

CC polypeptide designated as A, B, C or D or E, F, G, H or I. The bioactive molecule is a toxin, a radiolabel or an antibody. The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H, or I, or antibodies against them are useful for modulating a biological activity of a cell expressing a polypeptide designated as A, B, C or D or E, F, G, H, or I. The cell is killed. The proteins are useful for identifying agonists or antagonists, for the preparation of a medicament useful in the treatment of a condition which is responsive to the proteins, and as molecular weight markers for protein electrophoresis purposes, and as therapeutic agents for treating sports-related joint problems, CC articular cartilage defects, osteoarthritis or rheumatoid arthritis. CC Nucleic acids encoding the proteins are useful as hybridisation probes, CC in chromosome and gene mapping, in the generation of anti-sense RNA and CC DNA, for the preparation of the proteins, to generate transgenic or CC knockout animals which are useful in the development and screening of CC therapeutic useful reagents, for chromosome identification, and in gene CC therapy. The antibody is useful as a therapeutic agent, in a diagnostic CC assay and for affinity purification of the protein from recombinant CC cell culture natural sources. The present sequence represents a novel CC secreted or transmembrane protein of the invention.

XX Sequence 119 AA;

Query Match 100.0%; Score 119; DB 23; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-110;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLISLLLLPLMLSMVSSSLNPGVAGHGRDQASRRWLQEGGQCECKDWFLRAP 60

DB 1 MKVLISLLLLPLMLSMVSSSLNPGVAGHGRDQASRRWLQEGGQCECKDWFLRAP 60

QY 61 RRKMTVSGLPKQPCDHPKGNVKTTRHQRHKPKNSRACQQLKQCLRSFALPL 119

DB 61 RRKMTVSGLPKQPCDHPKGNVKTTRHQRHKPKNSRACQQLKQCLRSFALPL 119

RESULT 11

ABU71181
ID ABU71181 standard; Protein; 119 AA.

XX AC ABU71181;

XX DT 10-JUN-2003 (first entry)

XX DE Human PRO842 protein.

XX KW Human; PRO; secreted; transmembrane; cytostatic; TNF-alpha; blood;
KW tumour necrosis factor alpha release; chondrocyte cell; proliferation;
KW differentiation; tumour; gene therapy.

XX OS Homo sapiens.

XX PN US2003036143-A1.

XX PD 20-FEB-2003.

XX PF 02-JUL-2002; 2002US-0187600.

XX PR 16-SEP-1998; 98WO-US19330.

XX PR 07-OCT-1998; 98WO-US21141.

XX PR 01-DEC-1998; 98WO-US25108.

XX PR 08-MAR-1999; 99WO-US05028.

XX PR 14-MAY-1999; 99WO-US10733.

XX PR 02-JUN-1999; 99WO-US12252.

XX PR 01-SEP-1999; 99WO-US20111.

XX PR 15-SEP-1999; 99WO-US21090.

XX PR 01-DEC-1999; 99WO-US28301.

XX PR 02-DEC-1999; 99WO-US28551.

XX PR 30-DEC-1999; 99WO-US31274.

XX PR 05-JAN-2000; 2000WO-US00219.

XX PR 18-FEB-2000; 2000WO-US04341.

XX PR 22-FEB-2000; 2000WO-US04342.

XX PR 22-FEB-2000; 2000WO-US04414.

24-FEB-2000;	2000WO-US05004.	PR	15-MAY-1998;	98US-085700P.
01-MAR-2000;	2000WO-US05601.	PR	18-MAY-1998;	98US-086023P.
02-MAR-2000;	2000WO-US05841.	PR	22-MAY-1998;	98US-086339Z.
15-MAR-2000;	2000WO-US06884.	PR	22-MAY-1998;	98US-086486P.
30-MAR-2000;	2000WO-US08439.	PR	28-MAY-1998;	98US-087098P.
17-MAY-2000;	2000WO-US13705.	PR	28-MAY-1998;	98US-087208P.
22-MAY-2000;	2000WO-US14042.	PR	02-JUN-1998;	98US-087609P.
30-MAY-2000;	2000WO-US14941.	PR	02-JUN-1998;	98US-087759P.
02-JUN-2000;	2000WO-US15264.	PR	03-JUN-1998;	98US-087827P.
28-JUL-2000;	2000WO-US20710.	PR	04-JUN-1998;	98US-088025P.
24-AUG-2000;	2000WO-US23328.	PR	04-JUN-1998;	98US-088028P.
08-NOV-2000;	2000WO-US30952.	PR	04-JUN-1998;	98US-088029P.
01-DEC-2000;	2000WO-US32678.	PR	04-JUN-1998;	98US-088033P.
20-DEC-2000;	2000WO-US34956.	PR	04-JUN-1998;	98US-088326P.
28-FEB-2001;	2001WO-US06520.	PR	05-JUN-1998;	98US-088167P.
01-JUN-2001;	2001WO-US17800.	PR	05-JUN-1998;	98US-088202P.
20-JUN-2001;	2001WO-US19692.	PR	05-JUN-1998;	98US-088212P.
29-JUN-2001;	2001WO-US21066.	PR	05-JUN-1998;	98US-088217P.
09-JUL-2001;	2001WO-US21735.	PR	03-JUN-1998;	98US-088655P.
29-AUG-2001;	2001WO-US27099.	PR	10-JUN-1998;	98US-088722P.
18-SEP-1997;	97US-059263P.	PR	10-JUN-1998;	98US-088738P.
18-SEP-1997;	97US-059266P.	PR	10-JUN-1998;	98US-088740P.
17-OCT-1997;	97US-062250P.	PR	10-JUN-1998;	98US-088811P.
21-OCT-1997;	97US-063486P.	PR	10-JUN-1998;	98US-088824P.
24-OCT-1997;	97US-063120P.	PR	10-JUN-1998;	98US-088825P.
24-OCT-1997;	97US-063121P.	PR	10-JUN-1998;	98US-088826P.
28-OCT-1997;	97US-063540P.	PR	11-JUN-1998;	98US-088861P.
28-OCT-1997;	97US-063541P.	PR	11-JUN-1998;	98US-088863P.
28-OCT-1997;	97US-063544P.	PR	11-JUN-1998;	98US-088876P.
28-OCT-1997;	97US-063566P.	PR	12-JUN-1998;	98US-089090P.
31-OCT-1997;	97US-063734P.	PR	12-JUN-1998;	98US-089105P.
31-OCT-1997;	97US-063870P.	PR	16-JUN-1998;	98US-089512P.
13-NOV-1997;	97US-064103P.	PR	16-JUN-1998;	98US-089514P.
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10-SEP-1998; 98US-099812P.

Query Match 100.0%; Score 119; DB 24; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-110;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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JUL 12
J71518
ASU71518 standard; Protein; 119 AA.
ABU71518;
10-JUN-2003 (first entry)
Human secreted polypeptide PRO842.
Human; gene therapy; tumour; cancer.
Homo sapiens.
US2003013855-A1.
16-JAN-2003.
03-MAY-2002; 2002US-0063616.
30-DEC-1998; 98RX-0062142.
08-MAR-1999; 99WO-US05028.
14-MAY-1999; 99WO-US10733.
30-DEC-1999; 99WO-US31274.
18-FEB-2000; 2000WO-US04341.
01-MAR-2000; 2000WO-US05601.
02-MAR-2000; 2000WO-US05841.
21-MAR-2000; 2000WO-US07532.
22-MAY-2000; 2000WO-US14042.
03-JUN-2000; 2000WO-US15264.
24-AUG-2000; 2000WO-US23328.
10-NOV-2000; 2000WO-US30873.
01-DEC-2000; 2000WO-US32878.
20-DEC-2000; 2000WO-US34956.
28-FEB-2001; 2001WO-US06520.
01-JUN-2001; 2001WO-US17800.
14-MAY-1999; 99US-0311832.
25-AUG-1999; 99US-0380137.
25-AUG-1999; 99US-0380138.
25-AUG-1999; 99US-0380139.
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25-AUG-1999; 99US-0380142.
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12-NOV-1999; 99US-0423844.
22-AUG-2000; 2000US-0644848.
18-SEP-2000; 2000US-0644610.
18-SEP-2000; 2000US-0685350.
08-NOV-2000; 2000US-0709238.
20-DEC-2000; 2000US-0747259.
22-MAR-2001; 2001US-0816744.
10-MAY-2001; 2001US-0854208.
10-MAY-2001; 2001US-0854280.
30-MAY-2001; 2001US-0870574.
05-JUN-2001; 2001US-0874503.
29-JUN-2001; 2001US-0865599.
18-JUL-2001; 2001US-0908827.
06-DEC-2001; 2001US-0906867.

XX (GETH ) GENENTECH INC.
XX
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
XX WPI; 2003-330485/31.
XX N-PSDB; ACA58822.
XX
XX New isolated antibody specifically binding a PRO polypeptide, useful
PT for the preparation of a medicament for treating disorders with the
PT aberrant expression or activity of the PRO polypeptide, such as tumor
XX conditions and cancer -
XX
XX Disclosure; Page 93; 406pp; English.
XX
XX The invention relates to an antibody that binds to a polypeptide with a
CC fully defined sequence given in the specification. The methods and
CC compositions (containing antibodies that specifically bind a PRO
CC polypeptide) of the present invention are useful for the preparation of a
CC medicament for the treatment of disorders associated with the aberrant
CC expression or activity of the PRO polypeptide, such as tumour conditions
CC and cancer. They can also be used to generate transgenic or knockout
CC animals useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides and encoding nucleic acids can be used as
CC molecular weight markers for protein electrophoresis, chromosome
CC identification and tissue typing. The PRO polypeptides are useful to
CC induce angiogenesis e.g wound healing; in the treatment of sports-related
CC joint problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis; diabetes; hyperinsulinaemia and hypoinsulinaemia. The
CC antibodies may be used in various diagnostic, competitive binding and/or
CC immunoprecipitation assays. The present sequence represents the amino
CC acid sequence of a PRO polypeptide of the invention.
XX
XX Sequence 119 AA;

Query Match 100.0%; Score 119; DB 24; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-110;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKVLISSLLLLPLMLMSVSSSLNPGVARGHRRDQASRRWLQGGQCECKDWFRLAP 60
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DB 61 RRKFMVSLPKKQPCDHFKNVKTTHQHRHHPKPKHSRACQFLKQCLRSFALPL 119

RESULT 13
ABU71964
ID ABU71964 standard; Protein; 119 AA.
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XX AC ABU71964;
XX
XX 11-JUN-2003 (first entry)
DT
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Novel human secreted and transmembrane protein PRO842.

Human; secreted and transmembrane polypeptide;
chromosome mapping; gene mapping; transgenic animal; knockout animal;
therapeutic agent screening; chromosome identification; tissue typing;
gene therapy.

Homo sapiens.

US2003018183-A1.

23-JAN-2003.

01-MAY-2002; 2002US-0063512.

06-DEC-2001; 2001US-0006867.

(GETH) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

WPI; 2003-330984/31.
N-PSDB; ACA60375.

New secreted and transmembrane PRO polypeptides and nucleic acid
molecules encoding the polypeptides, useful in gene therapy or
preparing a medicament for treating a condition that is responsive to
the PRO polypeptide or antibody -

Disclosure; Fig 26; 409pp; English.

The invention describes novel isolated PRO polypeptides. The PRO
polypeptides or anti-PRO antibodies are useful in preparing a medicament
for treating a condition that is responsive to the PRO polypeptide or
antibody. The PRO nucleotide sequences may be used as hybridisation
probes in chromosome and gene mapping, or in generating antisense RNA
and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides,
in assays to identify other proteins or molecules involved in binding
reaction, to generate transgenic animals or knockout animals, which in
turn are useful in the development and screening of therapeutically
useful reagents, for chromosome identification, and tissue typing. The
PRO polypeptides and nucleic acid molecules are also useful in gene
therapy, and as molecular weight markers for protein electrophoresis
purposes. The anti-PRO antibodies may be used in diagnostic assays for
PRO, or for the affinity purification of PRO from recombinant cell
culture or natural sources. This is the amino acid sequence of a novel
human secreted and transmembrane PRO polypeptide.

Sequence 119 AA;

Query Match 100.0%; Score 119; DB 24; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-110;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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JLT 14
72121

ABU72121 standard; Protein; 119 AA.

ABU72121;

13-JUN-2003 (first entry)

Human PRO polypeptide #13.

Human; PRO polypeptide; secreted and transmembrane protein;
anti-PRO antibody; diagnostic assay; gene expression.

Homo sapiens.

US2003023042-A1.

30-JAN-2003.

01-MAY-2002; 2002US-0063502.

06-DEC-2001; 2001US-0006867.

(GETH) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

WPI; 2003-331484/31.
N-PSDB; ACA63385.

Novel monoclonal antibody that binds to secreted and transmembrane
polypeptide, useful for detecting and purifying the polypeptide and
also for treating conditions responsive to the antibody -

Disclosure; Fig 26; 408pp; English.

The present invention relates to the isolation of novel human PRO
polypeptides, and the polynucleotide sequences encoding them. The
PRO polypeptides are secreted and transmembrane proteins. The PRO
polypeptides and polynucleotides are useful for preparing a
medicament useful in the treatment of a condition responsive to
anti-PRO antibody. Anti-PRO antibodies are useful in diagnostic
assays for PRO, by detecting its expression in specific cells,
tissues or serum, and for affinity purification of PRO from
recombinant cell culture or natural sources. ABU72109-ABU72192
represent the human PRO polypeptides of the invention.

Sequence 119 AA;

Query Match 100.0%; Score 119; DB 24; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.3e-110;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQGGQCECKDWFLRAP 60

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61 RRKFTVSGLPKQKPCDHFKNVKKTRHQRHHRKPNKHSRACQOFLKQCQLRSFALPL 119

RESULT 15

ABU65638

ID ABU65638 standard; Protein; 119 AA.

XX ABU65638;

XX 19-MAY-2003 (first entry)

XX Human secreted/transmembrane protein, SEQ ID 140.

XX Human; PRO; secreted protein; transmembrane protein;
cytostatic; antiarthritic; osteopathic; adrenal tumour; lung tumour;
colon tumour; breast tumour; prostate tumour; rectal tumour;
cervical tumour; liver tumour; TNF-alpha release; arthritis;
tumour necrosis factor alpha; chondrocyte cell; bone disorder;
cartilage disorder; sports injury.

XX Homo sapiens.

OS

US2003036156-A1.
20-FEB-2003.
02-JUL-2002; 2002US-0188767.
16-SEP-1998; 98WO-US19330.
07-OCT-1998; 98WO-US21141.
01-DEC-1998; 98WO-US25108.
08-MAR-1999; 98WO-US05028.
14-MAY-1999; 98WO-US10733.
02-JUN-1999; 98WO-US1252.
01-SEP-1999; 98WO-US20111.
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01-DEC-1999; 98WO-US28301.
02-DEC-1999; 98WO-US28551.
05-DEC-1999; 98WO-US31274.
30-JAN-2000; 2000WO-US00219.
18-FEB-2000; 2000WO-US04341.
18-FEB-2000; 2000WO-US04342.
22-FEB-2000; 2000WO-US04414.
24-FEB-2000; 2000WO-US05004.
01-MAR-2000; 2000WO-US05601.
02-MAR-2000; 2000WO-US05841.
15-MAR-2000; 2000WO-US06884.
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28-FEB-2001; 2001WO-US06520.
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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	8	6.7	472	4	US-09-252-991A-22807
6	8	6.7	571	4	US-09-134-001C-3865
7	8	6.7	1015	4	US-09-285-385C-2
8	8	6.7	1023	2	US-08-475-891A-2
9	8	6.7	1023	2	US-08-567-375-2
10	8	6.7	1023	2	US-08-587-680A-2
11	7	5.9	31	1	US-08-090-036-1
12	7	5.9	38	4	US-09-390-134B-34
13	7	5.9	54	4	US-09-227-357-212
14	7	5.9	116	1	US-08-434-705B-6
15	7	5.9	116	2	US-09-086-201-6
16	7	5.9	129	1	US-08-434-705B-4
17	7	5.9	129	2	US-09-086-201-4
18	7	5.9	209	1	US-08-455-001-2
19	7	5.9	209	3	US-08-308-814-2
20	7	5.9	209	4	US-09-214-631-6
21	7	5.9	209	5	PCT-US95-11869-2
22	7	5.9	213	1	US-09-608-324A-10
23	7	5.9	213	2	US-08-920-440B-10
24	7	5.9	213	3	US-09-173-432-10
25	7	5.9	213	3	US-09-173-133-10
26	7	5.9	213	4	US-09-580-236A-10
27	7	5.9	230	2	US-08-471-371-2

Sequence 7, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 16901, A
Sequence 2, Appli
Sequence 2, Appli
Sequence 22552, A
Sequence 27879, A
Sequence 4, Appli
Sequence 2, Appli
Sequence 5, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 18540, A

ALIGNMENTS

RESULT 1

US-09-996-243-165

; Sequence 165, Application US/09996243

; Patent No. 6478825

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tamas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2730P1C13

; CURRENT APPLICATION NUMBER: US/09/996,243

; CURRENT FILING DATE: 2001-11-14

; PRIOR FILING DATE: 1997-06-16

; PRIOR FILING DATE: 1997-06-16

; PRIOR FILING DATE: 1997-10-17

; PRIOR FILING DATE: 1997-11-12

; PRIOR FILING DATE: 1997-11-13

; PRIOR FILING DATE: 1997-11-13

; PRIOR FILING DATE: 1997-11-24

; PRIOR FILING DATE: 1998-02-25

; PRIOR FILING DATE: 1998-03-20

; PRIOR FILING DATE: 1998-04-28

[illegible]

PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 119; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 4.3e-108;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRWLQEGQCECKDWFRLAP 60
|||||
1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRWLQEGQCECKDWFRLAP 60
|||||
61 RRKFTVSGLPKQPCDHPKGNVYKTRHQHHRKPNKHSRAQQFLKQCQLRSFALPL 119
|||||
61 RRKFTVSGLPKQPCDHPKGNVYKTRHQHHRKPNKHSRAQQFLKQCQLRSFALPL 119
|||||

ULT 2

08-171-299B-9
sequence 9, Application US/08171299B
atent No. 5599665

GENERAL INFORMATION:

APPLICANT: Barbieri, Joseph T.

APPLICANT: Frank, Dara W.

TITLE OF INVENTION: EXOENZYME S PROTEIN PREPARATION AND CLONED

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: QUARLES & BRADY

STREET: 411 East Wisconsin Avenue

CITY: Milwaukee

STATE: Wisconsin

COUNTRY: U.S.A.

ZIP: 53202-4497

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/171,299B

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Baker, Jean C.

REGISTRATION NUMBER: 35,433

REFERENCE/DOCKET NUMBER: 650053.90871

TELECOMMUNICATION INFORMATION:

TELEPHONE: (414) 277-5709

TELEFAX: (414) 271-3552

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

08-171-299B-9

Query Match 6.7%; Score 8; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

23 SLNPGVAR 30

|||||

13 SLNPGVAR 20

ULT 3

09-461-325-484

sequence 484, Application US/09461325A

; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/09/461,325A
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 484
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (84)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-461-325-484

Query Match 6.7%; Score 8; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SLLLPL 14

|||||

Db 24 SLLLPL 31

RESULT 4

US-08-788-231A-15

; Sequence 15, Application US/08788231A

; Patent No. 6019974

; GENERAL INFORMATION:

; APPLICANT: L'Hernault, Steven W.

; TITLE OF INVENTION: SPE-4 RELATED PEPTIDES, ANTIBODIES AND

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.

; STREET: 5370 Manhattan Circle, Suite 201

; CITY: Boulder

; STATE: Colorado

; COUNTRY: US

; ZIP: 80303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/788,231A

; FILING DATE: 24-JAN-1997

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/010,672

; FILING DATE: 26-JAN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Ferber, Donna M.

; REGISTRATION NUMBER: 33,878

REFERENCE/DOCKET NUMBER: 60-95

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 499-8080

TELEFAX: (303) 499-8089

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 462 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: not relevant

MOLECULE TYPE: protein

HYPOTHETICAL: YES

08-788-231A-15

Query Match 6.7%; Score 8; DB 3; Length 462;

Best Local Similarity 100.0%; Pred. No. 6.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 LISSLLLL 11

|||||

162 LISSLLLL 169

SULT 5

-09-252-991A-22807

Sequence 22807, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 22807

LENGTH: 472

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

-09-252-991A-22807

Query Match 6.7%; Score 8; DB 4; Length 472;

Best Local Similarity 100.0%; Pred. No. 6.3;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

23 SLNPGVAR 30

|||||

364 SLNPGVAR 371

SULT 6

-09-134-001C-3865

Sequence 3865, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 3865

LENGTH: 571

TYPE: PRT

ORGANISM: Staphylococcus epidermidis

US-09-134-001C-3865

Query Match

6.7%; Score 8; DB 4; Length 571;

Best Local Similarity 100.0%; Pred. No. 7.5;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LISSLLLL 11

|||||

Db 556 LISSLLLL 563

RESULT 7

US-09-285-385C-2

Sequence 2, Application US/09285385C

Patent No. 6579702

GENERAL INFORMATION:

APPLICANT: Greenspan, Daniel S.

APPLICANT: Scott, Ian C.

APPLICANT: Thomas, Christina L.

TITLE OF INVENTION: MAMMALIAN TOLLOID-LIKE GENE AND PROTEIN

FILE REFERENCE: 960296.96111

CURRENT APPLICATION NUMBER: US/09/285,385C

CURRENT FILING DATE: 1999-04-02

PRIOR APPLICATION NUMBER: 60/111873

PRIOR FILING DATE: 1998-12-11

PRIOR APPLICATION NUMBER: 60/080550

PRIOR FILING DATE: 1998-04-03

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 2

LENGTH: 1015

TYPE: PRT

ORGANISM: human

US-09-285-385C-2

Query Match

6.7%; Score 8; DB 4; Length 1015;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SLILLLPL 14

|||||

Db 12 SLILLLPL 19

RESULT 8

US-08-475-891A-2

Sequence 2, Application US/08475891A

Patent No. 5859339

GENERAL INFORMATION:

APPLICANT: Ronald, Pamela C.

APPLICANT: Wang, Guo-Liang

APPLICANT: Song, Wen-Yuang

TITLE OF INVENTION: Procedures and Materials for Conferring

TITLE OF INVENTION: Disease Resistance in Plants

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/475,891A

FILING DATE: 06-JUN-1995

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02370-058910US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1023 amino acids
TYPE: amino acid
STRADEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1023
OTHER INFORMATION: /note= "Xa21 Xanthomonas spp.
OTHER INFORMATION: disease resistance polypeptide RRK-F
OTHER INFORMATION: from rice (Oryza sativa)"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1010
OTHER INFORMATION: /note= "Xaa = Leu when position
OTHER INFORMATION: 5471 of RRK-F = G or Phe when position
OTHER INFORMATION: 5471 of RRK-F = C"
US-08-567-375-2
Query Match 6.7%; Score 8; DB 2; Length 1023;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
5 ISSLLLLL 12
|||||
10 ISSLLLLL 17

LT 9
US-567-375-2
Sequence 2, Application US/08567375
Patent No. 5952485
GENERAL INFORMATION:
APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for Conferring
DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/567,375
FILING DATE: 04-DEC-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-058930
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1023 amino acids
TYPE: amino acid
STRADEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1023
OTHER INFORMATION: /note= "Xa21 Xanthomonas spp. disease
OTHER INFORMATION: resistance polypeptide RRK-F from rice
OTHER INFORMATION: (Oryza sativa)"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1010
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = Leu when position 5471 of
OTHER INFORMATION: RRK-F = G or Phe when position 5471 of
OTHER INFORMATION: RRK-F = C"
US-08-567-375-2
Query Match 6.7%; Score 8; DB 2; Length 1023;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
5 ISSLLLLL 12
|||||
10 ISSLLLLL 17

RESULT 10
US-08-567-680A-2
Sequence 2, Application US/08587680A
Patent No. 5977434
GENERAL INFORMATION:
APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for Conferring
DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/587,680A
FILING DATE: 17-JAN-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/567,375
FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-058940US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1023 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1023
OTHER INFORMATION: /note= "Xa21 Xanthomonas spp. disease
OTHER INFORMATION: resistance polypeptide RRK-F from rice
OTHER INFORMATION: (Oryza sativa)"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1010
OTHER INFORMATION: /note= "Xaa = Leu when position 5471 of
OTHER INFORMATION: RRK-F = G or Phe when position 5471 of
OTHER INFORMATION: RRK-F = C"
-08-587-680A-2

Query Match 6.7%; Score 8; DB 2; Length 1023;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

5 ISSLLLLL 12
10 ISSLLLLL 17

SULT 11
-08-090-036-1
Sequence 1, Application US/08090036
Patent No. 5474922
GENERAL INFORMATION:
APPLICANT: Dotreich, Kurt
APPLICANT: Dalboge, Henrik
APPLICANT: Mikkelson, Jan M.
APPLICANT: Mischler, Marcel
APPLICANT: Christensen, Flemming M.
TITLE OF INVENTION: Beta-1,4-GALACTANASE AND A DNA SEQUENCE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5474922o No. 5474922disk of No. 5474922th America, Inc.
STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/090,036
FILING DATE: 15-JUL-1993
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK92/00037
FILING DATE: 06-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BE 91610007.6
FILING DATE: 06-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lowley Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 3564.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-867-0298
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Aspergillus aculeatus
STRAIN: CBS 101.43
US-08-090-036-1

Query Match 5.9%; Score 7; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ISSLLLL 11
DB 9 ISSLLLL 15

RESULT 12
US-09-390-134B-34
Sequence 34, Application US/09390134B
Patent No. 6518399
GENERAL INFORMATION:
APPLICANT: BARNES, ASHLEY A.
APPLICANT: WISE, ALAN
APPLICANT: MARSHALL, FIONA H.
APPLICANT: FRASER, NEIL J.
APPLICANT: WHITE, JULIE H. M.
APPLICANT: FOORD, STEVEN M.
TITLE OF INVENTION: NOVEL RECEPTOR
FILE REFERENCE: PG3558US2
CURRENT APPLICATION NUMBER: US/09/390,134B
CURRENT FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: GB9819420.2
PRIOR FILING DATE: 1998-09-07
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34
LENGTH: 38
TYPE: PRT
ORGANISM: Homo sapiens
US-09-390-134B-34

Query Match 5.9%; Score 7; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLLLLPL 14
DB 25 LLLLLPL 31

RESULT 13
US-09-227-357-212
Sequence 212, Application US/09227357

Patent No. 6342581
GENERAL INFORMATION:
APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: P2010P1
CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
ARLIER APPLICATION NUMBER: PCT/US98/13684
ARLIER FILING DATE: 1998-07-07
ARLIER APPLICATION NUMBER: 60/051,926
ARLIER FILING DATE: 1997-07-08
ARLIER APPLICATION NUMBER: 60/052,793
ARLIER FILING DATE: 1997-07-08
ARLIER APPLICATION NUMBER: 60/051,925
ARLIER FILING DATE: 1997-07-08
ARLIER APPLICATION NUMBER: 60/051,929
ARLIER FILING DATE: 1997-07-08
ARLIER APPLICATION NUMBER: 60/052,803
ARLIER FILING DATE: 1997-07-08
ARLIER APPLICATION NUMBER: 60/052,732
ARLIER FILING DATE: 1997-07-08
ARLIER APPLICATION NUMBER: 60/051,931
ARLIER FILING DATE: 1997-07-08
ARLIER APPLICATION NUMBER: 60/051,932
ARLIER FILING DATE: 1997-07-08
ARLIER APPLICATION NUMBER: 60/051,916
ARLIER FILING DATE: 1997-07-08
ARLIER APPLICATION NUMBER: 60/051,930
ARLIER FILING DATE: 1997-07-08
ARLIER APPLICATION NUMBER: 60/051,918
ARLIER FILING DATE: 1997-07-08
ARLIER APPLICATION NUMBER: 60/051,920
ARLIER FILING DATE: 1997-07-08
ARLIER APPLICATION NUMBER: 60/052,733
ARLIER FILING DATE: 1997-07-08
ARLIER APPLICATION NUMBER: 60/052,795
ARLIER FILING DATE: 1997-07-08
ARLIER APPLICATION NUMBER: 60/051,919
ARLIER FILING DATE: 1997-07-08
ARLIER APPLICATION NUMBER: 60/051,928
ARLIER FILING DATE: 1997-07-08
ARLIER APPLICATION NUMBER: 60/055,722
ARLIER FILING DATE: 1997-08-18
ARLIER APPLICATION NUMBER: 60/055,723
ARLIER FILING DATE: 1997-08-18
ARLIER APPLICATION NUMBER: 60/055,948
ARLIER FILING DATE: 1997-08-18
ARLIER APPLICATION NUMBER: 60/055,949
ARLIER FILING DATE: 1997-08-18
ARLIER APPLICATION NUMBER: 60/055,953
ARLIER FILING DATE: 1997-08-18
ARLIER APPLICATION NUMBER: 60/055,950
ARLIER FILING DATE: 1997-08-18
ARLIER APPLICATION NUMBER: 60/055,947
ARLIER FILING DATE: 1997-08-18
ARLIER APPLICATION NUMBER: 60/055,964
ARLIER FILING DATE: 1997-08-18
ARLIER APPLICATION NUMBER: 60/056,360
ARLIER FILING DATE: 1997-08-18
ARLIER APPLICATION NUMBER: 60/055,684
ARLIER FILING DATE: 1997-08-18
ARLIER APPLICATION NUMBER: 60/055,984
ARLIER FILING DATE: 1997-08-18
ARLIER APPLICATION NUMBER: 60/055,954
ARLIER FILING DATE: 1997-08-18
ARLIER APPLICATION NUMBER: 60/058,785
ARLIER FILING DATE: 1997-09-12
ARLIER APPLICATION NUMBER: 60/058,664
ARLIER FILING DATE: 1997-09-12
ARLIER APPLICATION NUMBER: 60/058,660
ARLIER FILING DATE: 1997-09-12
ARLIER APPLICATION NUMBER: 60/058,661
ARLIER FILING DATE: 1997-09-12

NUMBER OF SEQ ID NOS: 672
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 212
LENGTH: 54
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (54)
OTHER INFORMATION: Xaa equals stop translation
US-09-227-357-212

Query Match 5.9%; Score 7; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLLLLPL 14
Db 9 LLLLLPL 15

RESULT 14
US-08-434-705B-6
Sequence 6, Application US/08434705B
Patent No. 5798258
GENERAL INFORMATION:
APPLICANT: Douglass Ph.D., James
TITLE OF INVENTION: CART PROTEIN AND DNA ENCODING THEREFOR
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis K. Shelton
STREET: 1420 Fifth Avenue, Suite 2800
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,705B
FILING DATE: May 4, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
REFERENCE/DOCKET NUMBER: OHSUI8446
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-8100
TELEFAX: (206) 224-0779
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-434-705B-6

Query Match 5.9%; Score 7; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLLLLPL 14
Db 16 LLLLLPL 22

RESULT 15
US-09-086-201-6
Sequence 6, Application US/09086201

Thu Feb 19 08:38:56 2004

Patent No. 5969103
GENERAL INFORMATION:
APPLICANT: Douglass Ph.D., James
TITLE OF INVENTION: CART PROTEIN AND DNA ENCODING THEREFOR
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis K. Shelton
STREET: 1420 Fifth Avenue, Suite 2800
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/086,201
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/434,705
FILING DATE: May 4, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
REFERENCE/DOCKET NUMBER: OHSU18446
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-8100
TELEFAX: (206) 224-0779
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
-09-086-201-6
Query Match 5.9%; Score 7; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
8 LLLLLL 14
16 LLLLLL 22
Arch completed: February 18, 2004, 15:45:16
Time: 30 secs

Alt No.	Score	Query Match	Length	DB	ID	Description
1	119	100.0	119	9	US-09-989-722-165	Sequence 165, App
2	119	100.0	119	9	US-09-989-723-165	Sequence 165, App
3	119	100.0	119	9	US-09-989-279-165	Sequence 165, App
4	119	100.0	119	9	US-09-989-737-165	Sequence 165, App
5	119	100.0	119	10	US-09-989-731-165	Sequence 165, App
6	119	100.0	119	10	US-09-989-732-165	Sequence 165, App
7	119	100.0	119	10	US-09-989-073-165	Sequence 165, App
8	119	100.0	119	10	US-09-990-442-165	Sequence 165, App
9	119	100.0	119	10	US-09-991-163-165	Sequence 165, App
10	119	100.0	119	10	US-09-993-604-165	Sequence 165, App
11	119	100.0	119	10	US-09-990-456-165	Sequence 165, App
12	119	100.0	119	10	US-09-989-721-165	Sequence 165, App
13	119	100.0	119	10	US-09-992-598-165	Sequence 165, App
14	119	100.0	119	10	US-09-989-939A-165	Sequence 165, App
15	119	100.0	119	10	US-09-989-735-165	Sequence 165, App

Sequence 165, Application US/09989722
Patent No. US20020072067A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Garber, Hanspeter
APPLICANT: Gertschen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Gutowksi, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transferred
TITLE OF INVENTION: Acids Encoding
FILE REFERENCE: P2730PIC63
CURRENT APPLICATION NUMBER: US/09/989722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186
 PRIOR FILING DATE: 1997-11-12
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066770
 PRIOR FILING DATE: 1997-11-24
 PRIOR APPLICATION NUMBER: 60/075945
 PRIOR FILING DATE: 1998-02-25
 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/084500
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/087106
 PRIOR FILING DATE: 1998-05-28
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087609
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087759
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087827
 PRIOR FILING DATE: 1998-06-03
 PRIOR APPLICATION NUMBER: 60/088021
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088025
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088026
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088028
 PRIOR FILING DATE: 1998-06-04
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 PRIOR APPLICATION NUMBER: 60/088033
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088326
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 PRIOR APPLICATION NUMBER: 60/088167
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088202
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 PRIOR APPLICATION NUMBER: 60/088217
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088655
 PRIOR FILING DATE: 1998-06-09
 PRIOR APPLICATION NUMBER: 60/088734
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088738
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088742
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088810
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088824
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088826
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088858
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088861
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088876
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/089105
 PRIOR FILING DATE: 1998-06-12
 PRIOR APPLICATION NUMBER: 60/089440
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089512

PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Very Match 100.0%; Score 119; DB 9; Length 119;
1st Local Similarity 100.0%; Pred. No. 3.5e-101; Indels 0; Gaps 0;
Matches 119; Conservative 0; Mismatches 0;

1 MKVLISLLLLPLMLSMVSSSLNPGVARGHRRDRCQASRRMLQGGQCECKDWFLRAP 60
|||||
1 MKVLISLLLLPLMLSMVSSSLNPGVARGHRRDRCQASRRMLQGGQCECKDWFLRAP 60
|||||
61 RRKPMVSGLPKQCPCDHFKNVKKTRHQRHRRKNKHSRACQQLKQCQLRSFALPL 119
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61 RRKPMVSGLPKQCPCDHFKNVKKTRHQRHRRKNKHSRACQQLKQCQLRSFALPL 119
|||||

ILT 2

9-989-723-165
Sequence 165, Application US/09989723
Accession No. US20020072092A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

Acids Encoding the Same

TITLE REFERENCE: P273P1652

CURRENT APPLICATION NUMBER: US/09/989, 723

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
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PRIOR APPLICATION NUMBER: 60/088026
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PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
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PRIOR FILING DATE: 1998-06-23
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PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
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PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478

PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 119; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.5e-101;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLISLLLLPLMLMSVSSINFGVARGHRRDQASRRWLQEGQCECKDWFLRAP 60
DB 1 MKVLISLLLLPLMLMSVSSINFGVARGHRRDQASRRWLQEGQCECKDWFLRAP 60
QY 61 RRKFTVSGLPKKQPCDHFKNVKKTRHQRHRRKPKHSHRACQOFLKQCLRSFALPL 119
DB 61 RRKFTVSGLPKKQPCDHFKNVKKTRHQRHRRKPKHSHRACQOFLKQCLRSFALPL 119

RESULT 3
US-09-989-279-165
; Sequence 165, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C56
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24

[illegible]

PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

very Match 100.0%; Score 119; DB 9; Length 119;
est Local Similarity 100.0%; Pred. No. 3.5e-101;
atches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRRDGOASRWLQEGGQCECKDWFLRAP 60
|||||
1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRRDGOASRWLQEGGQCECKDWFLRAP 60
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61 RKFTVSGLPKQPCPDHFGKGVKTKTHQHHKPKNKHGRACQQLKQQLRSFALPL 119
|||||
61 RKFTVSGLPKQPCPDHFGKGVKTKTHQHHKPKNKHGRACQQLKQQLRSFALPL 119
|||||

ULT 4
09-989-727-165
sequence 165, Application US/09989727
Patent No. US20020072497A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: F2730PC65
CURRENT APPLICATION NUMBER: US/09/989,727
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1998-07-09
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Best Local Similarity 100.0%; Pred. No. 3.5e-101;
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Db 1 MKVLSSLLLLPLMLSMVSSSLNPGVARGHRDGGQARRWLQGGQCECKDWFLRAP 60
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RESULT 5
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; Sequence 165, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C70
; CURRENT APPLICATION NUMBER: US/09/989,731
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9-989-732-165
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APPLICANT: Ashkenazi, Avi J.
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APPLICANT: Botstein, David
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APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
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APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC57
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Query Match 100.0%; Score 119; DB 10; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.5e-101; Indels 0; Gaps 0;
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; Patent No. US20020127576A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Godowski, Paul J.
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; APPLICANT: Napier, Mary A.
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C15
; CURRENT APPLICATION NUMBER: US/09/991,073
; PRIOR FILING DATE: 2001-11-14
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Very Match 100.0%; Score 119; DB 10; Length 119;
1st Local Similarity 100.0%; Pred. No. 3.5e-101; Indels 0; Gaps 0;
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JLT 8

09-990-442-165
sequence 165; Application US/09990442

agent No. US20020122252A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnovers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

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APPLICANT: Goddard, Audrey

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APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

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APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

Acids Encoding the Same

FILE REFERENCE: P2730PIC8

CURRENT APPLICATION NUMBER: US/09/990,442

PRIOR FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

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R10R FILING DATE: 1998-07-09

Very Match 100.0%; Score 119; DB 10; Length 119;
1st Local Similarity 100.0%; Pred. No. 3.5e-101;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MKVLISLLLLPLMLSMVSSSLNPGVARGHRDRGASRRWLQEGGQCECKDWFLRAP 60
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DB 61 RRKFTVSGLPKQKQPCDHFKNYKTKTHQHHHRKPNKHSRACQOFLKQQLRSFALPL 119

RESULT 9

US-09-991-163-165
; Sequence 165, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC17
; CURRENT APPLICATION NUMBER: US/09/991,163
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-07-09

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Best Local Similarity 100.0%; Pred. No. 3.5e-101;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LT 10

9-993-604-165

Quence 165, Application US/09993604

tent No. US20020137075A1

NERAL INFORMATION:

PPPLICANT: Ashkenazi, Avi J.

PPPLICANT: Baker, Kevin P.

PPPLICANT: Botstein, David

PPPLICANT: Desnoyers, Luc

PPPLICANT: Eaton, Dan L.

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PPPLICANT: Wood, William I.

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

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Prior APPLICATION NUMBER: 60/092182
Prior FILING DATE: 1998-07-09

Query Match 100.0%; Score 119; DB 10; Length 119;
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Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 11

US-09-990-456-165
; Sequence 165, Application US/09990456
; Patent No. US20020137890A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C22
; CURRENT APPLICATION NUMBER: US/09/990,456
; CURRENT FILING DATE: 2001-11-14
; Prior APPLICATION NUMBER: 60/049787
; Prior FILING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 119; DB 10; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.5e-101;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ULI 12

09-989-721-165

sequence 165 Application US/09989721

agent No. US20020142961A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

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APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same

FILE REFERENCE: P2730PIC55

CURRENT APPLICATION NUMBER: US/09/989,721

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est Local Similarity 100.0%; Pred. No. 3.5e-101;
atches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 165, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 119; DB 10; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.5e-101; Indels 0; Gaps 0;
Matches 119; Conservative 0; Mismatches 0;

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RESULT 14
US-09-989-293A-165
; Sequence 165; Application US/09989293A
; Patent No. US20020177164A1

INTERNAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C66
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/0493787
PRIOR FILING DATE: 1997-06-16
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Query Match 100.0%; Score 119; DB 10; Length 119;
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SUIT 15
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 Sequence 165, Application US/09989735
 Publication No. US20020193299A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
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 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730PIC61
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R10R FILING DATE: 1998-07-09

Query Match 100.0%; Score 119; DB 10; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.5e-101; Indels 0; Gaps 0;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Search completed: February 18, 2004, 15:46:06
Job time : 35 secs

GenCore version 5.1.6
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rotein - protein search, using sw model

on: February 18, 2004, 15:34:55 ; Search time 21 Seconds
(without alignments)
544.956 Million cell updates/sec

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Gapop 60.0 , Gapext 60.0

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i size: 0

l number of hits satisfying chosen parameters: 283308

mm DB seq length: 0
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base: PIR 76:*

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2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	8	6.7	453	2	A53735
6	8	6.7	594	2	B90586
7	8	6.7	1305	2	AD0428
8	7	5.9	22	2	PH1333
9	7	5.9	52	2	AF0293
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11	7	5.9	107	2	S39207
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probable membrane
gene MAC25 protein
hypothetical prote
prostaglandin-simu
conserved hypothet
probable polynucle
trypsin homolog -
ABC transporter su
probable peroxidas
beta-N-acetyl-P-gl
hrpv protein - Pse

30 7 5.9 262 2 G90493

31 7 5.9 263 2 S57346

32 7 5.9 263 2 H86147

33 7 5.9 264 2 G90884

34 7 5.9 264 2 H85733

35 7 5.9 264 2 F64896

36 7 5.9 277 2 I52825

37 7 5.9 280 2 F96768

38 7 5.9 282 2 S50031

39 7 5.9 294 2 B71256

40 7 5.9 295 2 B83587

41 7 5.9 303 2 T13598

42 7 5.9 319 2 G82694

43 7 5.9 329 2 F94640

44 7 5.9 332 2 G83270

45 7 5.9 333 2 S61849

ALIGNMENTS

RESULT 1

C71549

hypothetical protein C71549 - Chlamydia trachomatis (serotype D, strain UW3/Cx)

C/Species: Chlamydia trachomatis

C/Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999

C/Accession: C71549

R/Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998

A/Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac

A/Reference number: A71570; MUID:99000809; PMID:9784136

A/Accession: C71549

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-86 <ARN>

A/Cross-references: GB:AE001290; GB:AE001273; NID:G3328560; PIDN:AAC67755.1; PID:G332856

A/Experimental source: serotype D, strain UW-3/Cx

C/Genetics:

A/Gene: C7164

Query Match 6.7%; Score 8; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ISLLLLLL 12

Db 46 ISLLLLLL 53

RESULT 2

B70037

hypothetical protein yvfA - Bacillus subtilis

C/Species: Bacillus subtilis

C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999

C/Accession: B70037

R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Brington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y, M.; Ogawa, K.; Ogihara, A.; Oudaga, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A/Authors: Schleitch, S.; Schreter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron ikeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tostato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, f A/Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A/Reference number: A69580; MUID:98044033; PMID:9384377

A/Accession: B70037

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

```

cucle type: DNA
esidues: 1-109 <KUN>
ross-references: GB:Z99121; GB:AL009126; NID:G2635827; PIDN:CAB15432.1; PID:el186115;
xperimental source: strain 168
enetics:
ene: yvfa

Query Match 6.7%; Score 8; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 SLLSLLPL 14
|||||
92 SLLSLLPL 99

ULT 3
ha-2-macroglobulin receptor-associated protein precursor - mouse
lternate names: heparin-binding protein-44
lternates: Mus musculus (house mouse)
ate: 19-May-1994 #sequence_revision 19-May-1994 #text_change 20-Jun-2000
cession: JX0281; JX0126
akamoto, M.; Ozawa, M.; Jacinto, S.D.; Furukawa, T.; Natori, Y.; Shirahama, H.; Yonez
Biochem. 114, 344-349, 1993
itle: Mouse heparin binding protein-44 (HBP-44) associates with brushin, a high-moled
reference number: JX0281; MUID:94110255; PMID:8282724
cession: JX0281
olecule type: mRNA
esidues: 1-360 <NAK>
ross-references: GB:S67967; NID:G460891; PIDN:AA0668.1; PID:G460892
urukawa, T.; Ozawa, M.; Huang, R.P.; Muramatsu, T.
Biochem. 108, 297-302, 1990
itle: A heparin binding protein whose expression increases during differentiation of
reference number: JX0126; MUID:91035363; PMID:2229028
cession: JX0126
olecule type: mRNA
esidues: 2-360 <FUR>
ross-references: GB:D00622; NID:G220433; PIDN:BA00500.1; PID:G220434
eywords: chondroitin sulfate proteoglycan; Glycoprotein; heparin binding
-37/Domain: signal sequence #status predicted <SIG>
8-360/Product: alpha-2-macroglobulin receptor-associated protein #status predicted <M
3.164/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
71/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.7%; Score 8; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

9 LLLSLLPL 16
|||||
19 LLLSLLPL 26

ULT 4
sory box histidine kinase [imported] - Caulobacter crescentus
pecies: Caulobacter crescentus
ate: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
cession: D87284
ierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Shapiro, J.C.; Fraser, C.M.
c. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
itle: Complete Genome Sequence of Caulobacter crescentus.
reference number: A87249; MUID:21173698; PMID:11259647
cession: D87284
tatus: preliminary
olecule type: DNA
esidues: 1-449 <STO>
ross-references: GB:AE005673; NID:G13421422; PIDN:AAK22272.1; GSPDB:GN00148
enetics:
ene: CC0285

```

```

Query Match 6.7%; Score 8; DB 2; Length 449;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 LLSLLLL 11
|||||
269 LLSLLLL 276

RESULT 5
A53735
exoenzyme S - Pseudomonas aeruginosa
NAlternate names: ADP-ribosyltransferase (EC 2.4.2.-); exoS
CSpecies: Pseudomonas aeruginosa
CDate: 07-Oct-1994 #sequence_revision 06-Oct-2000 #text_change 31-Dec-2000
CAccession: A53735; B83166
R.Kulich, S.M.; Yahr, T.L.; Mende-Mueller, L.M.; Barbieri, J.T.; Frank, D.W.
J. Biol. Chem. 269, 10431-10437, 1994
A>Title: Cloning the structural gene for the 49-kDa form of exoenzyme S (exoS) from Pse
AReference number: A53735; MUID:94193734; PMID:8144626
AAccession: A53735
A>Status: preliminary
AMolecule type: DNA
AResidues: 1-453 <KUL>
ACross-references: GB:L27629; NID:G639898; PIDN:AAA66491.1; PID:G450297
R.Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
AReference number: A82950; MUID:20437337; PMID:10984043
AAccession: B83166
A>Status: preliminary
AMolecule type: DNA
AResidues: 1-453 <STO>
ACross-references: GB:AE004801; GB:AE004091; NID:G9950011; PIDN:AAG07228.1; GSPDB:GN00
AExperimental source: strain PA01
CGenetics:
CKeywords: glycosyltransferase; pentosyltransferase

Query Match 6.7%; Score 8; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 SLNPGVAR 30
|||||
DB 345 SLNPGVAR 352

RESULT 6
B90586
transport protein sgat [imported] - Mycoplasma pulmonis (strain UAB CTIP)
CSpecies: Mycoplasma pulmonis
CDate: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
CAccession: B90586
R.Chanbaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galissen, F.; Moszer, I
Nucleic Acids Res. 29, 2145-2153, 2001
A>Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pul
AReference number: A99512; MUID:21267165; PMID:11353084
AAccession: B90586
A>Status: preliminary
AMolecule type: DNA
AResidues: 1-594 <KUR>
ACross-references: GB:AL445566; PID:G14090009; PIDN:CAC13767.1; GSPDB:GN00153
AExperimental source: strain UAB CTIP
CGenetics:
AGene: MIPU_5940
AGene: MIPU_5940
AGene: MIPU_5940
AGene: MIPU_5940

Query Match 6.7%; Score 8; DB 2; Length 594;
Best Local Similarity 100.0%; Pred. No. 7.7;

```


tches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3 VLISLL 10
|||||
231 VLISLL 238

LT 7
28
able exported protein YPO3523 [imported] - Yersinia pestis (strain CO92)
ecies: Yersinia pestis
te: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
cession: AD0428
khill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
re 413, 523-527, 2001
tle: Genome sequence of Yersinia pestis, the causative agent of plague.
ference number: AB0001; MUID:21470413; PMID:11586360
cession: AD0428
atus: preliminary
lecul type: DNA
sidues: 1-1305 <KUR>
oss-references: GB:AL590842; PIDN:CA092752.1; PID:G15981447; GSPDB:GN00175
ne: YPO3523
erfamily: ynfN protein
ery Match 6.7%; Score 8; DB 2; Length 1305;
st Local Similarity 100.0%; Pred. No. 15;
tches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3 VLISLL 10
|||||
299 VLISLL 306

LT 8
33
eavy chain DJ region (clone C238-133) - human (fragment)
ecies: Homo sapiens (man)
te: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
cession: PH1333
seerman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
xp. Med. 176, 1577-1581, 1992
tle: Predominance of fetal type DJH joining in young children with B precursor lymph
ference number: PH1302; MUID:93094761; PMID:1460419
cession: PH1333
lecul type: DNA
sidues: 1-22 <WAS>
ywords: heterotetramer; immunoglobulin

ery Match 5.9%; Score 7; DB 2; Length 22;
st Local Similarity 100.0%; Pred. No. 4.5;
tches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

7 SLLLLP 13
|||||
8 SLLLLP 14

LT 9
93
thetical protein YPO2405 [imported] - Yersinia pestis (strain CO92)
ecies: Yersinia pestis
te: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
cession: AF0293
khill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
re 413, 523-527, 2001
tle: Genome sequence of Yersinia pestis, the causative agent of plague.
ference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AF0293
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-52 <KUR>
A:Cross-references: GB:AL590842; PIDN:CA091210.1; PID:G15980400; GSPDB:GN00175
C:Genetics:
A:Gene: YPO2405

Query Match 5.9%; Score 7; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SLLLLP 13
|||||
Db 36 SLLLLP 42

RESULT 10
S26485
cytochrome P450 21A/B mutant fusion protein - human
N:Alternate names: steroid 21-monooxygenase
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 17-Aug-1995 #text_change 15-Feb-1996
C:Accession: S26485; S29672
R:Helmsberg, A.; Kofler, R.
submitted to the EMBL Data Library, March 1991
A:Reference number: S26484
A:Accession: S26485
A:Molecule type: DNA
A:Residues: 1-97 <HEL>
A:Cross-references: EMBL:X58901
A:Experimental source: leukocyte clone AGS 8-23
A>Note: an unequal cross-over mutation of the CYP21P pseudogene and CYP21 gene in a cong
A:Accession: S29672
A:Molecule type: DNA
A:Residues: 1-97 <HE2>
A:Cross-references: EMBL:X58908
C:Genetics:
A:Gene: CYP21P/CYP21
A:Map position: 6p21.3
A:Introns: 68/1
C:Keywords: fusion protein

Query Match 5.9%; Score 7; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLLLLP 14
|||||
Db 6 LLLLLP 12

RESULT 11
S39207
hypothetical protein 2 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 19-May-2000
C:Accession: I61221; S39207
R:Courty, Y.; Rosinski-Chupin, I.; Rougeon, F.
J. Biol. Chem. 269, 520-527, 1994
A:Title: A new proline-rich protein precursor expressed in the salivary glands of the ra
A:Reference number: A53118; MUID:94103265; PMID:8276845
A:Accession: I61221
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-107 <COU>
A:Cross-references: EMBL:X74229; NID:9433616; PIDN:CAA52301.1; PID:G433618
A>Note: submitted to the EMBL Data Library, July 1993
C:Comment: This is translated in an alternate reading frame of the proline-rich protein

Query Match 5.9%; Score 7; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

8 LLLLLL 14
|||||
10 LLLLLL 16

JUT 12
130
schematic protein F5982.10 - Caenorhabditis elegans
Species: Caenorhabditis elegans
ate: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 04-Mar-2000
cession: S31130
lston, J.; Du, Z.; Thomas, K.; Wilson, R.; Hillier, L.; Staden, R.; Halloran, N.; G
ias, T.; Ainscough, R.; Waterston, R.
mitted to the EMBL Data Library, November 1991
erification: The C. elegans sequencing project: A beginning.
ference number: S31122
cession: S31130
tatus: preliminary
olecule type: DNA
esidues: 1-117 <SUL>
ross-references: EMBL:Z11505; NID:G6718; PID:G6727
enetics:
ntrons: 21/2; 74/1
uperfamily: Caenorhabditis elegans hypothetical protein F5982.10

very Match 5.9%; Score 7; DB 2; Length 117;
est Local Similarity 100.0%; Pred. No. 19;
atches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

5 ISSLLLL 11
|||||
8 ISSLLLL 14

ULT 13
476
sine monophosphate cyclohydrolase homolog - Archaeoglobus fulgidus
pecies: Archaeoglobus fulgidus
ate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
cession: B69476
lenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
odek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
ure 390, 364-370, 1997
uthors: Otterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
th, H.O.; Woese, C.R.; Venter, J.C.
itle: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
ference number: A69250; MUID:98049343; PMID:9389475
cession: B69476
tatus: preliminary; nucleic acid sequence not shown; translation not shown
olecule type: DNA
esidues: 1-157 <KIE>
ross-references: GB:AE000378; GB:AE000782; NID:G2689301; PIDN:AAB89440.1; PID:G264873

Query Match 5.9%; Score 7; DB 2; Length 157;
est Local Similarity 100.0%; Pred. No. 24;
atches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MKVLISS 7
|||||
1 MKVLISS 7

ULT 14
744
ll T antigen - rhesus polyomavirus
pecies: Polyomavirus maccacae 1 (rhesus polyomavirus, SV40)
ate: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 22-Oct-1999
cession: C03631; C36763; A03618
eddy, V.B.; Thimmappaya, B.; Dhar, R.; Subramanian, K.N.; Zain, B.S.; Pan, J.; Ghosh,
ence 200, 494-502, 1978
itle: The genome of simian virus 40.

A;Reference number: A03631; MUID:78159686; PMID:205947
A;Accession: C03631
A;Molecule type: DNA
A;Residues: 1-174 <RED>
A;Cross-references: GB:J02400; GB:J02402; GB:J02403; GB:J02406; GB:J02407; GB:J02408; GE
35061
R;Piers, W.; Contreras, R.; Haegeman, G.; Rogiers, R.; van de Voorde, A.; van Heuverswy
Nature 273, 113-120, 1978
A;Title: Complete nucleotide sequence of SV40 DNA.
A;Reference number: A36763; MUID:78156432; PMID:205802
A;Accession: C36763
A;Molecule type: DNA
A;Residues: 1-174 <FIE>
A;Cross-references: GB:V01380; NID:G62000; PIDN:CAA24673.1; PID:G62005
A;Experimental source: strain 776
C;Comment: The initial 82 residues of the large T and small t antigens from SV40 are co
C;Superfamily: small t antigen; dnaJ amino-terminal homology
C;Keywords: acetylated amino end; early protein
F;12-62/Domain: dnaJ amino-terminal homology #status atypical <DNJ>
F;1/Modified site: acetylated amino end (Met) #status experimental

Query Match 5.9%; Score 7; DB 1; Length 174;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 SSLNPGV 28
|||||
DB 86 SSLNPGV 92

RESULT 15
A86363
hypothetical protein F19G10.14 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C;Accession: A86363
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K
ansen, N.F.; Hughes, B.; Ruizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A86363
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-187 <STO>
A;Cross-references: GB:AE005172; NID:G2462834; PIDN:AAB72169.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1

Query Match 5.9%; Score 7; DB 2; Length 187;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLLLLL 14
|||||
DB 6 LLLLLL 12

Search completed: February 18, 2004, 15:44:46
Job time : 34 secs

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GenCore version 5.1.6
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rotein - protein search, using sw model

on: February 18, 2004, 14:41:55 ; Search time 13 Seconds
(without alignments)
430.475 Million cell updates/sec

e: US-09-786-260-1

ect score: 119

ence: 1 MKVLISLLLLPLMLMSNV.....SRACQFLKQQLRSFALPL 119

ing table: OLIGO

Gapop 60.0 , Gapext 60.0

ched: 127863 seqs, 47026705 residues

(size : 0

l number of hits satisfying chosen parameters: 127863

mum DB seq length: 0

mum DB seq length: 2000000000

-processing: Listing first 45 summaries

base : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

ult	lc.	Score	Query Match	Length	DB	ID	Description
1	9	7.6	837	1	PHLD_MOUSE	O70362	mus musculus
2	8	6.7	360	1	AMRP_MOUSE	P55302	mus musculus
3	7	5.9	106	1	YKJ0_CAEEL	P34485	caenorhabdi
4	7	5.9	107	1	PRK2_RAT	O84113	rattus norv
5	7	5.9	128	1	PRK2_MOUSE	O98x17	mus musculus
6	7	5.9	129	1	CART_MOUSE	P56388	mus musculus
7	7	5.9	129	1	CART_RAT	P49192	rattus norv
8	7	5.9	145	1	RL2A_TRYBB	O15883	trypanosoma
9	7	5.9	154	1	RNS6_BOVIN	P08904	bos taurus
10	7	5.9	174	1	TASM_SV40	P03081	simian viru
11	7	5.9	202	1	YP37_DHIRA	O93rf5	deinococcus
12	7	5.9	203	1	YGINW_HAEIN	P44272	haemophilus
13	7	5.9	205	1	YK07_YEAST	P36061	saccharomyc
14	7	5.9	209	1	EFA2_MOUSE	P52801	mus musculus
15	7	5.9	211	1	CLDD_MOUSE	Q94084	mus musculus
16	7	5.9	213	1	EFA2_HUMAN	O43921	homo sapien
17	7	5.9	227	1	Y443_METJA	Q57885	methanococc
18	7	5.9	230	1	SGV1_MOUSE	Q98219	mus musculus
19	7	5.9	232	1	FL3L_MOUSE	P43772	mus musculus
20	7	5.9	245	1	CIQC_HUMAN	P02747	homo sapien
21	7	5.9	249	1	YBGO_STRCO	P40179	streptomyce
22	7	5.9	264	1	YDCV_ECOLI	P77505	escherichia
23	7	5.9	281	1	IBP7_MOUSE	Q61581	mus musculus
24	7	5.9	282	1	IBP7_HUMAN	Q16270	homo sapien
25	7	5.9	329	1	PE18_ARATH	Q98k52	arabidopsis
26	7	5.9	332	1	NAGZ_PSEAE	Q98k52	arabidopsis
27	7	5.9	339	1	SRG7_CAEEL	P54129	pseudomonas
28	7	5.9	350	1	GAN4_ASPAC	P48842	aspergillus
29	7	5.9	364	1	CD33_HUMAN	P20138	homo sapien
30	7	5.9	367	1	DIAC_RAT	Q01460	rattus norv
31	7	5.9	372	1	CD14_RABIT	Q28680	oryctolagus
32	7	5.9	375	1	CD14_HUMAN	P08571	homo sapien
33	7	5.9	388	1	OPUL_HUMAN	Q98488	homo sapien

ALIGNMENTS

RESULT 1

PHLD_MOUSE

ID PHLD_MOUSE STANDARD; PRT; 837 AA.

AC O70362;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Phosphatidylinositol-glycan-specific phospholipase D 1 precursor

DE (EC 3.1.4.50) (PI-G PLD) (Glycoprotein phospholipase D) (Glycosyl-

DE phosphatidylinositol specific phospholipase D).

GN GPLDL

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Glucagonoma;

RX MEDLINE=98384535; PubMed=9716655;

RA LeBoeuf R.C., Caldwell M., Guo Y., Metz C., Davitz M.A., Olson L.K.,

Deeg M.A.;

RT "Mouse glycosylphosphatidylinositol-specific phospholipase D (Gpld1)

characterization."

RL Mamm. Genome 9:710-714 (1998).

CC -I- FUNCTION: This protein hydrolyzes the inositol phosphate linkage

in proteins anchored by phosphatidylinositol glycans (GPI-anchor)

thus releasing these proteins from the membrane.

CC -I- CATALYTIC ACTIVITY: 6-(alpha-D-glucosaminyl)-1-phosphatidyl-1D-

myo-inositol + H(2)O = 6-(alpha-D-glucosaminyl)-1D-myo-inositol +

phosphatidate.

CC -I- SUBCELLULAR LOCATION: Secreted.

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CC EMBL; AF050666; AAC77799.1; -

DR MGD; MGI:106604; Gpld1

DR GO; GO:0008507; P:GPI anchor release; IDA.

DR InterPro; IPR001028; Gpdt_Plipased.

DR InterPro; IPR000413; Integrin_alpha.

DR Pfam; PF01839; FG-GAP; 4.

DR PRINTS; PR00718; PHPLIPASED.

DR SMART; SM00191; Int alpha; 5.

DR Hydrolase; Glycoprotein; Signal.

FT SIGNAL 1 23

FT CHAIN 24 837

FT BY SIMILARITY

FT PROPHATIDYLINOSITOL-GLYCAN-SPECIFIC

FT PHOSPHOLIPASE D 1.

FT CARBOHYD 94 94

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 267 267

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 287 287

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 303 303

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

Best Local Similarity	100.0%;	Pred. No. 3.7;	
Matches	8;	Conservative	0;
Mismatches	0;	Indels	0;
Gaps	0;	Gaps	0;

RESULT 3
YMJ0_CAEEL
ID_YMJ0_CAEEL STANDARD; PRT; 106 AA.

DT	01-FEB-1994	(Rel. 28
DT	28-FEB-2003	(Rel. 41
DT	28-FEB-2003	(Rel. 41

OS *Caenorhabditis elegans*.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
NCBI_TaxID=6239;
RX [1]_
RN SEQUENCE FROM N.A.
RP STRAIN=Bristol N2.
RC
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Letreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.

RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
 RA Watson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
 RA Whitehead P.,
 RT 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans,"
 RT Nature 368:32-38(1994).
 RL [2]
 RN REVISIONS.
 RP

RA Durbin, R.;
 CC Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -----
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CC
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DR
DR
DR
KW
FT

EMBL; Zil505; CAA77587.2; -
WormPep; F59B2.10; CE28835.
Hypothetical protein.
DOMAIN 11 14
POLY-LEU.

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or send an email to license@sib-sib.ch).

Query Match
Best Local Similarity

Matches	5	ISSLLLL	11
Qy			

Db 8 ISSLLLL 14

RESULT 4		
PRK2 RAT		
ID PRK2 RAT	STANDARD;	PRT; 107 AA
AC 08R413:		

DT 28-FEB-2003 (Rel. 41, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)
Prokineticin 2 precursor (PK2).
PROK2.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley;
MEDLINE=22050031; PubMed=12054613;
Masuda Y., Takatsu Y., Terao Y., Kumano S., Ishibashi Y., Suenaga M.,
Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S.,
Inatomi N., Ohkaki T., Onda H., Fujino M.;
"Isolation and identification of EG-VEGF/prokineticins as cognate
ligands for two orphan G-protein-coupled receptors.";
Biochem. Biophys. Res. Commun. 293:396-402(2002).
[2]
EFFECT ON CIRCADIAN LOCOMOTOR ACTIVITY.
MEDLINE=22022134; PubMed=12024206;
Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J.,
Weaver D.R., Leslie F.M., Zhou Q.-Y.;
"Prokineticin 2 transmits the behavioural circadian rhythm of the
suprachiasmatic nucleus";
Nature 417:405-410(2002).
-1- FUNCTION: May function as an output molecule from the
suprachiasmatic nucleus (SCN) that transmits behavioral circadian
rhythm. May also function locally within the SCN to synchronize
output. Potentially contracts gastrointestinal (GI) smooth muscle (By
similarity).
-1- SUBUNIT: Binds to PKR1 and PKR2, both are G-protein coupled
receptors.
-1- SUBCELLULAR LOCATION: Secreted (By similarity).
-1- TISSUE SPECIFICITY: Expressed at high levels in testis and at
lower levels in brain, lung, ovary, spleen, thymus and uterus.
-1- INDUCTION: Activated by Clock and Bmal1 heterodimers and light;
inhibited by period genes (PER1, PER2 and PER3) and cryptochrome
genes (CRY1 and CRY2) (Probable).
-1- SIMILARITY: BELONGS TO THE PROKINETICIN FAMILY.

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EMBL; AY089984; AAM09105.1; -
Neuropeptide; Biological rhythms; Signal.
SIGNAL 1 26
CHAIN 27 107 PROKINETICIN 2.
DISULFID 33 45 BY SIMILARITY.
DISULFID 39 57 BY SIMILARITY.
DISULFID 44 85 BY SIMILARITY.
DISULFID 67 93 BY SIMILARITY.
DISULFID 87 103 BY SIMILARITY.
SEQUENCE 107 AA; BDFF316DCB5FED0 CRC64;
Very Match 5.9%; Score 7; DB 1; Length 107;
atches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
8 LLLLLL 14
| | | | |
11 LLLLLL 17
JLT 5
} MOUSE
} PKR2 MOUSE STANDARD; PRT; 128 AA.
Q9QXU7; Q9QXU5; Q9QXU6;
16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Prokineticin 2 precursor (PK2) (Protein Bv8 homolog).
DE PROK2 OR Bv8.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RN STRAIN=129/SV;
RC MEDLINE=20047850; PubMed=10580115;
RX Wechselberger C., Puglisi R., Lepperdinger G., Boitani C., Kreil G.;
RA "The mammalian homologue of Bv8 from frog skin is mainly expressed in
RT spermatocytes.";
RL FEBS Lett. 462:177-181(1999).
[2]
SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RN STRAIN=129/SVJ;
RC MEDLINE=20510004; PubMed=11054548;
RX Jilek A., Engel E., Beier D., Lepperdinger G.;
RA "Murine Bv8 Gene maps near a syntenic breakpoint of mouse chromosome 6
RT and human 3p21.";
RL Gene 256:189-195(2000).
[3]
SEQUENCE FROM N.A. (ISOFORM 2), AND FUNCTION.
RN STRAIN=C57BL/6;
RC MEDLINE=22022134; PubMed=12024206;
RX Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J.,
RA Weaver D.R., Leslie F.M., Zhou Q.-Y.;
RT "Prokineticin 2 transmits the behavioural circadian rhythm of the
RT suprachiasmatic nucleus";
RL Nature 417:405-410(2002).
[4]
SEQUENCE FROM N.A. (ISOFORM 1).
RN STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=21085660; PubMed=11217851;
RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Azakawa K., Izawa M., Nihi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,
RA Hayashizaki Y.;
RL "Functional annotation of a full-length mouse cDNA collection.";
CC Nature 409:685-690(2001).
CC -1- FUNCTION: May function as an output molecule from the
CC suprachiasmatic nucleus (SCN) that transmits behavioral circadian
CC rhythm. May also function locally within the SCN to synchronize
CC output. Potentially contracts gastrointestinal (GI) smooth muscle (By
CC similarity).
CC -1- SUBUNIT: Binds to PKR1 and PKR2, both are G-protein coupled
CC receptors.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=Bv8-a;
CC IsoId=Q9QXU7-1; Sequence=Displayed;
CC Names=2; Synonyms=Bv8-b;
CC IsoId=Q9QXU7-2; Sequence=VSP_005220;
CC Names=3;
CC IsoId=Q9QXU7-3; Sequence=VSP_005221;

```

-!- TISSUE SPECIFICITY: Expressed in the SCN and among a few other
discrete brain areas, including the islands of Calleja, media 1
prosopic area of the hypothalamus and the shell of the nucleus
accumbens. Highly expressed in testis. In the SCN, expression
subjected to high amplitude of circadian oscillation.
-!- DEVELOPMENTAL STAGE: Expressed in mid-late pachytene spermatocytes
at the stages VII, VIII and IX of the semiferous epithelial cycle.
-!- INDUCTION: Activated by Clock and Bmal heterodimers and light;
inhibited by period genes (PER1, PER2 and PER3) and cryptochrome
genes (CRY1 and CRY2).
-!- SIMILARITY: BELONGS TO THE PROKINECTIN FAMILY.
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EMBL; AF182064; AAF15259.1; -
EMBL; AF182065; AAF15260.1; -
EMBL; AF182066; AAF15261.1; -
EMBL; AF182067; AAG09439.1; -
EMBL; AF182067; AAG09439.1; JOINED.
EMBL; AF487280; AAM49572.1; -
EMBL; AK015462; BAB29857.1; -
HSSP; P25687; IIMT.
MGD; MGI:1354178; Prok2.
Neuropeptide; Biological rhythms; Signal; Alternative splicing.
POTENTIAL.
CHAIN 1 26
PROKINETICIN 2.
DISULFID 33 45
BY SIMILARITY.
DISULFID 39 57
BY SIMILARITY.
DISULFID 44 106
BY SIMILARITY.
DISULFID 67 114
BY SIMILARITY.
DISULFID 108 124
BY SIMILARITY.
VARSPPLIC 74 94
Missing (in isoform 2).
/FTID=VSP 005220.
SHVANGROERRRKRKRKKEVPWGRMRHHTCPCLPGLAC
isoform 3)
LRTSNFRICLARK -> VSVCTGILGVPSH (in
isoform 3)
/FTID=VSP 005221.
SEQUENCE 128 AA; 14185 MW; 5F08BA177FDDB58C CRC64;

Query Match 5.9%; Score 7; DB 1; Length 128;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

8 LLLLLL 14
|||||
11 LLLLLL 17

ULT 6
RT MOUSE
CART_MOUSE STANDARD; PRT; 129 AA.
P56388; Q9QXZ8;
15-JUL-1998 (Rel. 36, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cocaine- and amphetamine-regulated transcript protein precursor
[Contains: CART(1-52); CART(55-102)].
CART.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
STRAIN=129/SvJ;
MEDLINE=20080750; PubMed=10612705;
Adams L.D., Gong W., Vechia S.D., Hunter R.G., Kuhar M.J.;

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RT "CART: from gene to function.";
RL Brain Res. 848:137-140(1999).
CC -!- FUNCTION: Satiety factor closely associated with the actions of
CC leptin and neuropeptide Y; this anorectic peptide inhibits both
CC normal and starvation-induced feeding and completely blocks the
CC feeding response induced by neuropeptide Y and regulated by leptin
CC in the hypothalamus (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Names=Long;
CC IsoId=P56388-1; Sequence=Displayed;
CC Names=Short;
CC IsoId=P56388-2; Sequence=VSP 000793;
CC -!- SIMILARITY: BELONGS TO THE CART FAMILY.
-----
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EMBL; AF148071; AAF24168.1; -
DR HSSP; Q16568; 1HY9.
DR MGD; MGI:1351330; Cart.
KW Neuropeptide; Neurotransmitter; Cleavage on pair of basic residues;
KW Alternative splicing; Signal.
FT SIGNAL 1 27
FT CHAIN 28 129
POTENTIAL.
COCAINE- AND AMPHETAMINE-REGULATED
TRANSCRIPT PROTEIN.
FT PEPTIDE 28 79
CART(1-52) (BY SIMILARITY).
FT PEPTIDE 82 129
CART(55-102) (BY SIMILARITY).
FT PEPTIDE 89 129
CART(62-102) (POTENTIAL).
FT DISULFID 95 113
BY SIMILARITY.
FT DISULFID 101 121
BY SIMILARITY.
FT DISULFID 115 128
BY SIMILARITY.
FT VARSPPLIC 54 66
Missing (in isoform Short).
/FTID=VSP 000793.
SEQUENCE 129 AA; 14285 MW; E4CA6CE70BEE6DF2 CRC64;

Query Match 5.9%; Score 7; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 LLLLLL 14
|||||
DB 16 LLLLLL 22

RESULT 7
CART RAT
ID CART RAT STANDARD; PRT; 129 AA.
AC P49192;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cocaine- and amphetamine-regulated transcript protein precursor
DE [Contains: CART(1-52); CART(55-102)].
GN CART.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
STRAIN=Sprague-Dawley; TISSUE=Brain;
RC MEDLINE=95198122; PubMed=7891182;
RA Douglass J.O., McKinzie A.A., Couceyro P.;
RT "PCR differential display identifies a rat brain mRNA that is
transcriptionally regulated by cocaine and amphetamine.";
RT J. Neurosci. 15:2471-2481(1995).

```

[2] SEQUENCE OF 81-97, MASS SPECTROMETRY, AND DISULFIDE BONDS.
MEDLINE=98316718; PubMed=9654146;
Thim L., Nielsen P.F., Judge M.E., Andersen A.S., Diers I.,
Egel-Mitani M., Hastrup S.;
"Purification and characterisation of a new hypothalamic satiety
peptide, cocaine and amphetamine regulated transcript (CART),
produced in yeast.";
FEBS Lett. 428:263-268(1998).
-!- FUNCTION: Satiety factor closely associated with the actions of
leptin and neuropeptide Y; this anorectic peptide inhibits both
normal and starvation-induced feeding and completely blocks the
feeding response induced by neuropeptide Y and regulated by leptin
in the hypothalamus (By similarity).
-!- SUBCELLULAR LOCATION: Secreted (Potential).
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=Long;
IsoId=P49192-1; Sequences=Displayed;
Name=Short;
IsoId=P49192-2; Sequences=VSP 000794;
-!- TISSUE SPECIFICITY: Neuroendocrine tissues. Predominantly
expressed in the hypothalamus, pituitary, and longitudinal muscle-
myenteric plexus. Abundant expression is also seen in the
midbrain/thalamus and eye. A lower level expression is seen in the
other brain regions and adrenal.
-!- INDUCTION: By cocaine and amphetamine.
-!- SIMILARITY: BELONGS TO THE CART FAMILY.

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EMBL; U10071; AAA87897.1; -;
HSP; Q16568; 1HY9.
Neuropeptide; Neurotransmitter; Cleavage on pair of basic residues;
Alternative splicing; Signal.
SIGNAL 1 27 POTENTIAL.
CHAIN 28 129 COCAINE- AND AMPHETAMINE-REGULATED
TRANSCRIPT PROTEIN.
PEPTIDE 28 79
PEPTIDE 82 129 CART(1-52).
PEPTIDE 89 129 CART(55-102).
DISULFID 95 113 CART(62-102) (POTENTIAL).
DISULFID 101 121
DISULFID 115 128
VARSPIC 54 66 Missing (in isoform Short).
SEQUENCE 129 AA; 14140 MW; 0FDE283705BB2728 CRC64;
/Frid=VSP_000794.
Query Match 5.9%; Score 7; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

8 LLLLLL 14
| | | | |
16 LLLLLL 22

LIT 8
TRYBB
R2A_TRYBB STANDARD; PRT; 145 AA.
O15883;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
60S ribosomal protein L27a (L29).
REL27A.
Trypanosoma brucei brucei.

OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Treu 667;
RA Brown S.V., Williams N.;
RT "The 60S ribosomal protein L27a (L29) gene of Trypanosoma brucei.";
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE L15P FAMILY OF RIBOSOMAL PROTEINS.

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CC EMBL; U96757; AAB62182.1; -;
DR InterPro; IPR001196; Ribosomal_L15.
DR Pfam; PF00256; L15; 1.
DR PROSITE; PS00475; RIBOSOMAL_L15; FALSE_NEG.
KW Ribosomal protein.
SQ SEQUENCE 145 AA; 16294 MW; DAC63E602D706D7C CRC64;
Query Match 5.9%; Score 7; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 85 KKTRHOR 91
DB 6 KKTRHOR 12

RESULT 9
RNS6_BOVIN STANDARD; PRT; 154 AA.
ID RNS6_BOVIN
AC P08904; Q95324; Q9TUP9;
DT 01-NOV-1988 (Rel. 09, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease K6 precursor (EC 3.1.27.-) (RNase K6) (K6b) (RNase K2).
GN RNASE6 OR RNS6 OR RK6B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Spinal cord.
RA Pietrowski D., Foerster M.;
RT "Complete cDNA sequence of a bovine ribonuclease k6b (brk6b).";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 28-154.
RX MEDLINE=89034023; PubMed=3182769;
RA Irie M., Nitta R., Ohgi K., Niwata Y., Watanabe H., Iwama M.,
RA Beintema J.J., Senda A., Takizawa Y.;
RT "Primary structure of a non-secretory ribonuclease from bovine
kidney.";
RL J. Biochem. 104:289-296(1988).
RN [3]
RP SEQUENCE OF 28-154.
RC Tissue=Kidney;
RX MEDLINE=85261183; PubMed=3926759;
RA Niwata Y., Ohgi K., Senda A., Takizawa Y., Irie M.;
RT "Purification and properties of bovine kidney ribonucleases.";
RL J. Biochem. 97:923-934(1985).
RN [4]
RP SEQUENCE OF 37-129 FROM N.A.
RX MEDLINE=96433147; PubMed=8836175;
RA Rosenberg H.F., Dyer K.D.;

"Molecular cloning and characterization of a novel human ribonuclease (Rnase k6): increasing diversity in the enlarging ribonuclease gene family." ;

Nucleic Acids Res. 24:3507-3513 (1996).

-1- FUNCTION: PYRIMIDINE SPECIFIC NUCLEASE WITH A PREFERENCE FOR U.
-1- SUBCELLULAR LOCATION: LYCOSOMAL (PROBABLE); MATRIX OF EOSINOPHIL'S
-1- LARGE SPECIFIC GRANULE.

-1- TISSUE SPECIFICITY: Kidney.

-1- SIMILARITY: Belongs to the pancreatic ribonuclease family.

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EMBL; AF164025; AAD44349.1; -.

EMBL; U64997; AAC48633.1; -.

PIR; S72363; S72363.

HSRP; P00656; 2RNS.

InterPro; IPR001427; RNaseA.

PRINTS; PF00074; rnaseA; 1.

PRINTS; PR00794; RIBONUCLEASE.

ProDom; P000535; RNaseA; 1.

SMART; SM00092; RNaseA; 1.

SMART; SM00092; RNaseA; 1.

PROSITE; PS00127; RNASE_PANCREATIC; 1.

Hydrolase; Nuclease; Endonuclease; Glycoprotein; Signal.

SIGNAL

CHAIN 28 154 RIBONUCLEASE K6.

ACT_SITE 42 42 BY SIMILARITY.

ACT_SITE 65 65 BY SIMILARITY.

ACT_SITE 149 149 BY SIMILARITY.

DISULFID 50 108 BY SIMILARITY.

DISULFID 64 118 BY SIMILARITY.

DISULFID 82 133 BY SIMILARITY.

DISULFID 89 96 BY SIMILARITY.

CARBOHYD 59 59 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 104 104 N-LINKED (GLCNAC. .) (POTENTIAL).

CONFLICT 45 51 PRLQCN -> SRLPQS (IN REF. 3).

CONFLICT 65 65 K -> N (IN REF. 4).

CONFLICT 153 154 VV -> YF (IN REF. 2 AND 3).

SEQUENCE 154 AA; 17660 MW; 9325DF841EF39C11 CRC64;

Query Match 5.9%; Score 7; DB 1; Length 154;
est Local Similarity 100.0%; Pred. No. 16;
atches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

6 SLLLLLL 12

|||||

9 SLLLLLL 15

ULT 10

M_SV40

TASM SV40

STANDARD;

PRT; 174 AA.

P03081;

21-JUL-1986 (Rel. 01, Created)

21-JUL-1986 (Rel. 01, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

Small T antigen. (SV40).

Simian virus 40 (SV40).

Viruses; GEDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.

NCBI_TaxID=10633;

[1]

SEQUENCE FROM N.A.

MEDLINE=78159686; PubMed=205947;

Reddy V.B., Thimmapaya B., Dhar R., Subramanian K.N., Zain B.S.,

Pan J., Ghosh P.K., Celma M.L., Weissman S.M.;

"The genome of simian virus 40.";

Science 200:494-502(1978).

[2]

RP SEQUENCE FROM N.A.
RC STRAIN=776;
RX MEDLINE=78156432; PubMed=205802;
RA Fiers W., Contreras R., Haegeman G., Rogiers R., van de Voorde A.,
van Heuverswyn H., van Herreweghe J., Volckaert G., Ysebaert M.;
RT "Complete nucleotide sequence of SV40 DNA.";
RL Nature 273:113-120(1978).
RN [3]
RP INHIBITION OF PHOSPHATASE PP2A ACTIVITY.
RX MEDLINE=91172186; PubMed=1848668;
RA Scheidtmann K.H., Mumby M.C., Rundell K., Walter G.;
RT "Dephosphorylation of simian virus 40 large-T antigen and p53 protein
by protein phosphatase 2A: inhibition by small-t antigen.";
RL Mol. Cell. Biol. 11:1996-2003(1991).
RN [4]
RP BINDING IN VITRO TO PP2A.
RX MEDLINE=91172185; PubMed=1706474;
RA Yang S.-L., Lickteig R.L., Estes R., Rundell K., Walter G.,
Mumby M.C.;
RT "Control of protein phosphatase 2A by simian virus 40 small-t
antigen.";
RL Mol. Cell. Biol. 11:1988-1995(1991).
RN [5]
RP -1- SUBUNIT: BINDS IN VITRO TO PP2A AND INTERACTS WITH THE A SUBUNIT
AND THIS INTERACTION INHIBITS ENZYME ACTIVITY.
CC -1- MISCELLANEOUS: THE INITIAL 82 RESIDUES OF THE LARGE T AND SMALL T
ANTIGENS FROM SV40 ARE CODED BY THE SAME NUCLEOTIDE SEQUENCE.
CC -1- SIMILARITY: Contains 1 J domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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EMBL; J02400; AAB59925.1; -.
PIR; C03631; TVVPA4.
InterPro; IPR001623; DnaJ N.
InterPro; IPR001354; Papo_T_antigen.
DR Pfam; PF00236; DnaJ; 1.
DR Pfam; PF02380; Papo_T_antigen; 1.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DnaJ_1; FALSE_NEG.
DR PROSITE; PS50076; DnaJ_2; 1.
DR Early protein; Acetylation.
KW DOMAIN 12 75 J-DOMAIN.
FT MOD_RES 1 1 ACETYLATION.
SQ SEQUENCE 174 AA; 20449 MW; 91EC925ED2E29668 CRC64;

Query Match 5.9%; Score 7; DB 1; Length 174;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 SSLNPGV 28
|||||
Db 86 SSLNPGV 92

RESULT 11
YP37 DEIRA
ID YP37 DEIRA STANDARD; PRT; 202 AA.
AC Q98FE5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein PR2537.
GN DR2537.
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]

SEQUENCE FROM N.A.
 STRAIN=RA / ATCC 13939 / DSM 20539 / NCIB 9279;
 MEDLINE=20036896; PubMed=10567266;
 White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 Makarewicz J.J., Lam P., McDonald L., Utterback T., Zaleski C.,
 Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 Fraser C.M.;
 "genome sequence of the radioresistant bacterium Deinococcus
 radiodurans R1";
 Science 286:1571-1577 (1999).
 -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 -1- SIMILARITY: BELONGS TO THE UPF0191 FAMILY.

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 EMBL; AB002083; AF12078.1; -;
 PIR; A75261; A75261.
 TIGR; DR2537; -;
 HAMAP; MF 01207; -; 1.
 Pfam; PF05252; UPF0191; 1.
 Hypothetical protein; Transmembrane; Complete proteome.
 TRANSMEM 9 31 POTENTIAL.
 TRANSMEM 46 68 POTENTIAL.
 TRANSMEM 80 99 POTENTIAL.
 TRANSMEM 114 133 POTENTIAL.
 TRANSMEM 146 168 POTENTIAL.
 TRANSMEM 173 190 POTENTIAL.
 SEQUENCE 202 AA; 22026 MW; 3D7AE477694736B CRC64;

 Query Match 5.9%; Score 7; DB 1; Length 202;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 8 LLLLLLPL 14
 |||||
 123 LLLLLLPL 129

RT
 RT Rd";
 RL Science 269:496-512 (1995).
 CC -1- SIMILARITY: STRONG, TO E. COLI YGIM.

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 CC EMBL; U32834; AAC23249.1; -;
 DR PIR; C64038; C64038.
 DR TIGR; H11605; -;
 DR InterPro; IPR003646; SH3_bac.
 DR SMART; SM0287; SH3b; 1.
 KW Hypothetical protein; Transmembrane; Signal; Complete proteome.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 203 HYPOTHETICAL PROTEIN H11605.
 FT TRANSMEM 167 189 POTENTIAL.
 SQ SEQUENCE 203 AA; 23112 MW; FAFCS5229FD29C05 CRC64;

 Query Match 5.9%; Score 7; DB 1; Length 203;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 4 LISSULL 10
 |||||
 Db 8 LISSULL 14

 RESULT 13
 YK07 YEAST STANDARD; PRT; 205 AA.
 ID YK07 YEAST
 AC P36051;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE Hypothetical 22.7 kDa protein in SDH1-CIMS/YTA3 intergenic region.
 GN YKL147C OR YKL601.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c;
 RX MEDLINE=94378720; PubMed=8091859;
 RA Vandenbol M., Bolle P.-A., Dion C., Portetelle D., Hilger F.;
 RT "DNA sequencing of a 36.2 kb fragment located between the PAS1 and
 LAP loci of chromosome XI of Saccharomyces cerevisiae.";
 RL Yeast 10:S35-S40 (1994).

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 CC EMBL; Z26877; CAA81507.1; -;
 DR PIR; Z28146; CAA81987.1; -;
 DR PIR; Z37804; S37804.
 DR SGD; S0001630; YKL147C.
 KW Hypothetical protein.
 SQ SEQUENCE 205 AA; 22673 MW; 01F1625B361D9DCE CRC64;

 Query Match 5.9%; Score 7; DB 1; Length 205;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

8 LLLLLLPL 14
 |||||
 78 LLLLLLPL 84

ULT 14
 2 MOUSE

EFNA2 MOUSE STANDARD; PRT; 209 AA.
 P52801;
 01-OCT-1996 (Rel. 34, Created)
 01-OCT-1996 (Rel. 34, Last sequence update)
 30-MAY-2000 (Rel. 39, Last annotation update)
 Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
 (LERK-6) (ELF-1) (CEK7-ligand) (CEK7-L).
 EFNA2 OR EPLG6 OR LERK6 OR ELF1 OR EPL6.
 Mus musculus (Mouse).
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]

SEQUENCE FROM N.A.
 STRAIN=Swiss Webster; TISSUE=Brain;
 MEDLINE=95007776; PubMed=7522971;
 Cheng H.J., Flanagan J.G.;
 "Identification and cloning of ELF-1, a developmentally expressed
 ligand for the Mek4 and Sek receptor tyrosine kinases.";
 Cell 79:157-168(1994).
 [2]

SEQUENCE FROM N.A.
 TISSUE=Brain;
 MEDLINE=95181289; PubMed=7876076;
 Shao H., Lou L., Pandey A., Verderame M.F., Siever D.A., Dixit V.M.;
 "cDNA cloning and characterization of a Cek7 receptor
 protein-tyrosine kinase ligand that is identical to the ligand
 (ELF-1) for the Mek-4 and Sek receptor protein-tyrosine kinases";
 J. Biol. Chem. 270:3467-3470(1995).

-1- SUBUNIT: BINDS TO THE RECEPTOR TYROSINE KINASES EFHA3, EFHA4 AND EFHA5.

-1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (Potential).

-1- SIMILARITY: BELONGS TO THE EPHRIN FAMILY.

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EMBL; U14941; AAA53636.1; -
 EMBL; U14752; AAA68520.1; -
 PIR; A54984; A54984.
 MGD; MGI:102707; Efna2.
 InterPro; IPR001799; Ephrin.
 Pfam; PF00812; Ephrin; 1.
 PRINTS; PR01347; EPHRIN.
 ProDom; PD002533; Ephrin; 1.
 PROSITE; PS01299; EPHRIN; 1.
 Glycoprotein; GPI-anchor; Signal.
 SIGNAL 1 20 POTENTIAL.
 CHAIN 21 209 EPHRIN-A2.
 CARBOHYD 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CARBOHYD 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SEQUENCE 209 AA; 23586 MW; F1997545F25B9ABC CRC64;

Query Match 5.9%; Score 7; DB 1; Length 209;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

8 LLLLLLPL 14

Db 12 LLLLLLPL 18

RESULT 15

CLDD MOUSE STANDARD; PRT; 211 AA.
 AC Q920S4;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Claudin-13.
 GN CLDN13.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]

SEQUENCE FROM N.A.

RA Morita K., Furuse M., Tsukita S;
 RA Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

RL [2]

SEQUENCE FROM N.A.

RA STRAIN=C57BL/6J; TISSUE=Embryonic liver;
 RA MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Flechner C., Fujita M., Gariboldi M.,
 RA Guscinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nardone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RA Nature 409:685-690(2001).
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the claudin family.

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EMBL; AF124428; AAD17322.1; -
 DR EMBL; AK010869; BAB27234.1; -
 DR MGD; MGI:1913102; Cldn13.
 DR InterPro; IPR006188; Claudin sup.
 DR InterPro; IPR004031; PMP22 Claudin.
 DR Pfam; PF00822; PMP22 Claudin; 1.
 DR PROSITE; PS01346; CLAUDIN; 1.
 DR Tight junction; Transmembrane
 FT TRANSMEM 9 29 POTENTIAL.
 FT TRANSMEM 81 101 POTENTIAL.
 FT TRANSMEM 119 139 POTENTIAL.
 FT TRANSMEM 166 186 POTENTIAL.
 SQ SEQUENCE 211 AA; 23503 MW; 53CC8697C53D46BE CRC64;

Query Match 5.9%; Score 7; DB 1; Length 211;
 Best Local Similarity 100.0%; Pred. No. 20;

ches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

6 SLLLLL 12

|||||

169 SLLLLL 175

h completed: February 18, 2004, 15:44:22
ime : 82 secs

GenCore version 5.1.6
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otein - protein search, using sw model

n: February 18, 2004, 15:31:05 ; Search time 34 Seconds
(without alignments)
903.184 Million cell updates/sec

ct score: 119
nce: 1 MKVLISLLLLPLMLMSV.....SRACQFLKQCLRSFALPL 119

ng table: OLIGO
Gapop 60.0 , Gapext 60.0

hed: 830525 seqs, 258052604 residues

size : 0
l number of hits satisfying chosen parameters: 830525

num DB seq length: 0

num DB seq length: 2000000000

rocessing: listing first 45 summaries

ase :

- 1: SPTREMBL 23:*
- 2: sp_archea:*
- 3: sp_bacteria:*
- 4: sp_fungi:*
- 5: sp_human:*
- 6: sp_invertebrate:*
- 7: sp_mammal:*
- 8: sp_mhc:*
- 9: sp_oxganelle:*
- 10: sp_page:*
- 11: sp_plant:*
- 12: sp_rhizobium:*
- 13: sp_virus:*
- 14: sp_unclassified:*
- 15: sp_rv:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

lt	Score	Query Match	Length	DB	ID	Description
1	13	10.9	128	11	Q8R3U6	Q8R3U6 mus musculus
2	9	7.6	309	16	Q8EV11	Q8EV11 mycoplasma
3	9	7.6	842	11	Q8R432	Q8R432 mus musculus
4	9	7.6	842	11	Q8DBH3	Q8DBH3 mus musculus
5	9	7.6	842	11	Q8VCU2	Q8VCU2 mus musculus
6	8	6.7	86	16	Q84166	Q84166 Chlamydia t
7	8	6.7	109	16	P71060	P71060 bacillus su
8	8	6.7	181	10	Q9FJN3	Q9FJN3 arabidopsis
9	8	6.7	182	10	Q8L625	Q8L625 arabidopsis
10	8	6.7	277	2	O69120	O69120 burkholderi
11	8	6.7	277	2	O9AEV4	O9AEV4 burkholderi
12	8	6.7	285	2	O33629	O33629 eaccharopol
13	8	6.7	332	8	Q8RHE7	Q8RHE7 chiroxiphia
14	8	6.7	360	11	Q8C252	Q8C252 mus musculus
15	8	6.7	363	11	Q8K295	Q8K295 mus musculus
16	8	6.7	384	16	Q8ESE3	Q8ESE3 oceanobacil

17	8	6.7	408	16	Q92QTS	Q92QTS rhizobium m
18	8	6.7	449	16	Q9ABE3	Q9ABE3 caulobacter
19	8	6.7	453	2	Q93SO0	Q93SO0 pseudomonas
20	8	6.7	453	2	Q93SP9	Q93SP9 pseudomonas
21	8	6.7	453	2	Q93SQ2	Q93SQ2 pseudomonas
22	8	6.7	453	2	Q93J5	Q93J5 pseudomonas
23	8	6.7	453	2	Q93SQ3	Q93SQ3 pseudomonas
24	8	6.7	453	2	Q93SQ3	Q93SQ3 pseudomonas
25	8	6.7	453	2	Q93SQ1	Q93SQ1 pseudomonas
26	8	6.7	453	16	Q51449	Q51449 pseudomonas
27	8	6.7	494	17	Q8U246	Q8U246 pyrococcus
28	8	6.7	594	16	Q8BXP5	Q8BXP5 mycoplasma
29	8	6.7	613	8	Q8HM93	Q8HM93 bregmaceros
30	8	6.7	827	16	Q8CPL9	Q8CPL9 scaphylococ
31	8	6.7	896	5	Q94891	Q94891 drosophila
32	8	6.7	1015	4	Q9Y6L7	Q9Y6L7 homo sapien
33	8	6.7	1236	3	Q9G105	Q9G105 schizosacch
34	8	6.7	1305	16	Q8ZB96	Q8ZB96 versinia pe
35	7	5.9	41	8	Q8HE48	Q8HE48 thraxan acu
36	7	5.9	41	8	Q8HE47	Q8HE47 thraxan ebe
37	7	5.9	52	16	Q8ZDY9	Q8ZDY9 versinia pe
38	7	5.9	68	10	Q8RYJ4	Q8RYJ4 oryza sativ
39	7	5.9	76	13	Q8JJ66	Q8JJ66 oncorhynch
40	7	5.9	89	10	Q8S6T9	Q8S6T9 oryza sativ
41	7	5.9	89	11	Q9WUG8	Q9WUG8 mus musculu
42	7	5.9	90	4	Q9UQV8	Q9UQV8 homo sapien
43	7	5.9	90	17	Q8U0W3	Q8U0W3 pyrococcus
44	7	5.9	92	10	Q9AS65	Q9AS65 oryza sativ
45	7	5.9	94	11	Q8K323	Q8K323 rattus norv

ALIGNMENTS

RESULT 1

Q8R3U6 PRELIMINARY; PRT; 128 AA.
ID Q8R3U6;
AC Q8R3U6;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Similar to hypothetical gene LOC125944.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024561; AAH24561.1; -
SQ SEQUENCE 128 AA; 14043 MW; CCE67DA04D23D7DF CRC64;

Query Match 10.9%; Score 13; DB 11; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 EGGQECCKDWFL 57
DB 45 EGGQECCKDWFL 57

RESULT 2

Q8EV11 PRELIMINARY; PRT; 309 AA.
ID Q8EV11;
AC Q8EV11;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Conserved hypothetical protein.
GN MPE7560.
OS Mycoplasma penetrans.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.

```

NCBI_TaxID=28227;
[1]
SEQUENCE FROM N.A.
STRAIN=HF-2;
MEDLINE=22354719; PubMed=12466555;
Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,
Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
"The complete genomic sequence of Mycoplasma penetrans, an
intracellular bacterial pathogen in humans.";
Nucleic Acids Res. 30:5293-5300(2002).
EMBL; AF04173; BAC4550.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 309 AA; 36285 MW; 045179015A472DD9 CRC64;

Query Match 7.6%; Score 9; DB 16; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 LISSLLLLL 12
|||||
171 LISSLLLLL 179

JLT 3
132 Q8R432 PRELIMINARY; PRT; 842 AA.
Q8R432;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Glycosylphosphatidylinositol phospholipase D.
GPI1.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
TISSUE=Liver;
Lund T., Flores-Borja F.;
"Characterization of the mouse glycosylphosphatidylinositol
phospholipase D (GPI-PLD gene).";
Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AY081194; AAL87452.1; -.
MGD; MGI:106604; Gpld1.
InterPro; IPR000413; Integrin_alpha.
Pfam; PF01833; FG-GAP; 6.
SMART; SM00191; Int_alpha; 5.
SEQUENCE 842 AA; 93653 MW; 2458B409EB515CD2 CRC64;

Query Match 7.6%; Score 9; DB 11; Length 842;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

JLT 4
833 Q9DBH3 PRELIMINARY; PRT; 842 AA.
Q9DBH3;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 20, Last annotation update)
Glycosylphosphatidylinositol specific phospholipase D1.
GPI1.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
TISSUE=Liver;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
Sakai K., Okido I., Furuno M., Aono H., Baidarelli R., Barsh G.,
Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring K., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
Hayaishizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AK004957; BAB23698.1; -.
MGD; MGI:106604; Gpld1.
InterPro; IPR001028; Gprt_Plipased.
DR Pfam; PF01839; FG-GAP; 6.
DR PRINTS; PR00718; PHPLIPASED.
DR SMART; SM00191; Int_alpha; 5.
SQ SEQUENCE 842 AA; 93646 MW; 119B25C835545533 CRC64;

Query Match 7.6%; Score 9; DB 11; Length 842;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 SSLLLLLPL 14
|||||
Db 8 SSLLLLLPL 16

RESULT 5
Q8VCU2 PRELIMINARY; PRT; 842 AA.
ID Q8VCU2
AC Q8VCU2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Glycosylphosphatidylinositol specific phospholipase D1.
GN GPLD1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
EN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019146; AAR19146.1; -.
DR MGD; MGI:106604; Gpld1.
DR InterPro; IPR001028; Gprt_Plipased.
DR Pfam; PF01839; FG-GAP; 4.
DR PRINTS; PR00718; PHPLIPASED.
DR SMART; SM00191; Int_alpha; 5.
SQ SEQUENCE 842 AA; 93623 MW; 2458B409EB550DD2 CRC64;

Query Match 7.6%; Score 9; DB 11; Length 842;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 SSLLLLLPL 14

```

8 SSLLLLLPL 16

LT 6

O84166 PRELIMINARY; PRT; 86 AA.

O84166; MEDLINE=99000809; PubMed=9784136;

01-NOV-1998 (TrEMBLrel. 08, Created)

01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

Hypothetical protein CT164.

CT164.

Chlamydia trachomatis.

Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.

NCBI_TaxID=813;

[1] _TaxID=813;

SEQUENCE FROM N.A.

STRAIN=D/UN-3/Cx;

MEDLINE=99000809; PubMed=9784136;

Stephens R.S., Kalman S., Lamm C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V., Davis R.W.;

"Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis."

Science 282:754-759(1998).

EMBL; AB001290; AAC67755.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 86 AA; 9162 MW; 55ED2981A0237F9B CRC64;

ery Match 6.7%; Score 8; DB 16; Length 86;

st Local Similarity 100.0%; Pred. No. 2.4;

atches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

5 ISSLLLLL 12

46 ISSLLLLL 53

LT 7

P71060 PRELIMINARY; PRT; 109 AA.

P71060; O08179;

01-FEB-1997 (TrEMBLrel. 02, Created)

01-FEB-1997 (TrEMBLrel. 02, Last sequence update)

01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

Hypothetical protein yvfa.

yvfa.

Bacillus subtilis.

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

NCBI_TaxID=1423;

[1]

SEQUENCE FROM N.A.

STRAIN=168TRP;

Fabret C., Quentin Y., Chapal N., Guiseppi A., Haiech J., Denizot F.;

Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.

[2]

SEQUENCE FROM N.A.

Denizot F.C.;

Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.

[3]

SEQUENCE FROM N.A.

STRAIN=168;

MEDLINE=98044033; PubMed=9384377;

Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Duserchot A., Ehrlich S.D., Emerson P.T., Etian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Gallizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A., Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mael C., Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Parro V., Pohl T.M., Portelle D., Porwollik S., Prescott A.M., Presecan E., Pujic P., Putelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Torkuchi M., Tamakoshi A., Tanaka T., Terpetra P., Tognoni A., Tosato V., Uchiyama S., Vanderbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;

"The complete genome sequence of the gram-positive bacterium Bacillus subtilis."

Nature 390:249-256(1997).

[4]

SEQUENCE FROM N.A.

STRAIN=168;

Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;

Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; 271928; CAA96478.1; -.

DR EMBL; 294043; CAB07994.1; -.

DR EMBL; 299121; CAB15432.1; -.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 109 AA; 12046 MW; F0C5F36DE3BD3D68 CRC64;

Query Match 6.7%; Score 8; DB 16; Length 109;

Best Local Similarity 100.0%; Pred. No. 2.9; 0; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0;

QY 7 SLLLLLPL 14

DB 92 SLLLLLPL 99

RESULT 8

Q9FJM3 PRELIMINARY; PRT; 181 AA.

AC Q9FJM3;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Phytoeyanin/early nodulin-like protein.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsais.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Columbia;

RX MEDLINE=98403884; PubMed=9734815;

RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N., Tabata S.;

RA "Structural analysis of Arabidopsis thaliana chromosome 5. VI. Sequence features of the regions of 1,367,185 bp covered by 19 physically assigned pl and TAC clones."

RL DNA Res. 5:203-216(1998).

DR EMBL; AB013396; BAB08862.1; -.

DR HSSP; P00303; 2CBP.

DR InterPro; IPR003245; Pcyvanin like.

DR Pfam; PF02298; Cu bind like; 1.

DR ProDom; PD003122; Pcyvanin like; 1.

SQ SEQUENCE 181 AA; 20216 MW; DCE3EE93CAED921 CRC64;

Query Match 6.7%; Score 8; DB 10; Length 181;

st Local Similarity 100.0%; Pred. No. 4.5; DB 10; Length 182;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 7 SLLLLLPL 14
 170 SLLLLLPL 177

LT 9
 Q8L625 PRELIMINARY; PRT; 182 AA.

Q8L625; 01-OCT-2002 (TREMBlrel. 22, Created)
 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 Phytoeyanin/early nodulin-like protein.
 AT5G5920.
 Arabidopsis thaliana (Mouse-ear cross).
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 NCBI_TaxID=3702;
 [1]

SEQUENCE FROM N.A.
 Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
 Palm C.J., Bowser L., Jones T., Bath J., Carrinci P., Chen H.,
 Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
 Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
 Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
 Ecker J., Theologis A., Davis R.W.;
 Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 EMBL: AY140062; AAM98203.1; -;
 InterPro; IPR003245; Plicyanin-like.
 Pfam; PF02298; Cu_bind-like; 1.
 ProDom; PD003122; Plicyanin like; 1.
 SEQUENCE 182 AA; 20343 MW; AA120684C34207CB CRC64;

Query Match 6.7%; Score 8; DB 10; Length 182;
 Best Local Similarity 100.0%; Pred. No. 4.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

7 SLLLLLPL 14
 171 SLLLLLPL 178

ULT 10
 O69120 PRELIMINARY; PRT; 277 AA.

O69120; 01-AUG-1998 (TREMBlrel. 07, Created)
 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 Putative ABC-2 transporter integral membrane component.
 WZM
 Burkholderia pseudomallei (Pseudomonas pseudomallei).
 Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 Burkholderiaceae; Burkholderia.
 NCBI_TaxID=28450;
 [1]

SEQUENCE FROM N.A.
 STRAIN-1026b;
 MEDLINE-99141012; PubMed-9988493;
 DeShazer D., Brett P.J., Woods D.E.;
 "The type II O-antigenic polysaccharide moiety of Burkholderia
 pseudomallei lipopolysaccharide is required for serum resistance and
 virulence."
 Mol. Microbiol. 30:1081-1100(1998).
 EMBL: AF064070; AAD05458.1; -;
 InterPro; IPR000412; ABC_transp2.
 Pfam; PF01061; ABC2_membrane; 1.
 PRINTS; PR00164; ABC2TRNSPORT.
 SEQUENCE 277 AA; 30644 MW; 01E50FFEE7378BF7 CRC64;

Query Match 6.7%; Score 8; DB 2; Length 277;
 Best Local Similarity 100.0%; Pred. No. 6.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 11 LLPLMLMS 18
 165 LLPLMLMS 172

RESULT 11
 Q9AEV4 PRELIMINARY; PRT; 277 AA.

Q9AEV4; 01-JUN-2001 (TREMBlrel. 17, Created)
 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 Putative ABC-2 transporter integral membrane component.
 WZM.
 Burkholderia mallei (Pseudomonas mallei).
 Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 Burkholderiaceae; Burkholderia.
 NCBI_TaxID=13373;
 [1]
 SEQUENCE FROM N.A.
 Burtinck M.N., Brett P.J., Woods D.E.;
 "Physical and Molecular Characterization of Lipopolysaccharide O-
 antigens from Burkholderia mallei";
 Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 EMBL: AY028370; AAK27395.1; -;
 InterPro; IPR000412; ABC_transp2.
 Pfam; PF01061; ABC2_membrane; 1.
 PRINTS; PR00164; ABC2TRNSPORT.
 SEQUENCE 277 AA; 30628 MW; ASA50FFEE7379636 CRC64;

Query Match 6.7%; Score 8; DB 2; Length 277;
 Best Local Similarity 100.0%; Pred. No. 6.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LLPLMLMS 18
 Db 165 LLPLMLMS 172

RESULT 12
 O33629 PRELIMINARY; PRT; 285 AA.

O33629; 01-JAN-1998 (TREMBlrel. 05, Created)
 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE ORF homologous to Escherichia coli and Salmonella typhimurium dnaE
 gene (Fragment).
 OS Saccharopolyspora erythraea (Streptomyces erythraeus).
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Pseudonocardineae; Pseudonocardaceae; Saccharopolyspora.
 OX NCBI_TaxID=1836;
 RN [1]_TaxID=1836;
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92121109; PubMed-1732208;
 RA Andersen J.F., Hutchinson C.R.;
 "Characterization of Saccharopolyspora erythraea cytochrome P-450
 RT genes and enzymes, including 6-deoxyerythronolide B hydroxylase";
 J. Bacteriol. 174:725-735(1992).
 RL EMBL; M83110; AAA26482.1; -;
 DR NON-IER 1
 FT SEQUENCE 285 AA; 30109 MW; EA741E79E4782B36 CRC64;

Query Match 6.7%; Score 8; DB 2; Length 285;
 Best Local Similarity 100.0%; Pred. No. 6.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 ARGHRDRG 36

|||||||
147 ARGHRDGR 154

LT 13
E7
Q8H77 PRELIMINARY; PRT; 332 AA.
01-MAR-2003 (T-EMBLrel. 23, Created)
01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
Cytochrome b (Fragment).
CYTB.
Chiroxiphia caudata.
Mitochondrion.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Pipridae; Chiroxiphia.
NCBI_TaxID=196027;
[1]
SEQUENCE FROM N.A.
Johansson U.S., Irestedt M., Parsons T.J., Ericson P.G.P.;
"Basal phylogenetic relationships within Tyrannidae";
Auk 0:0-0(2002). AN76175.1; -.
EMBL; AF453819; AN76175.1; -.
Mitochondrion.
NON TER 1
SEQUENCE 332 AA; 37577 MW; C037BC61B1CC00A2 CRC64;
Query Match 6.7%; Score 8; DB 8; Length 332;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q8K295 PRELIMINARY; PRT; 363 AA.
Q8K295;
01-OCT-2002 (T-EMBLrel. 22, Created)
01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032170; AAH32170.1; -.
DR InterPro; IPR000886; ER target.
DR PROSITE; PS00014; ER_TARGET; 1.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 363 AA; 42592 MW; 436A91BA9D75D1C5 CRC64;
Query Match 6.7%; Score 8; DB 11; Length 363;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LLLPLML 16
DB 22 LLLPLML 29

Search completed: February 18, 2004, 15:44:14
Job time : 48 secs

LT 14
:52
Q8C252 PRELIMINARY; PRT; 360 AA.
Q8C252;
01-MAR-2003 (T-EMBLrel. 23, Created)
01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
Low density lipoprotein receptor-related protein associated protein
1.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN=NOD;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs";
Nature 420:563-573(2002).
EMBL; AK089250; BAC40814.1; -.
SEQUENCE 360 AA; 42157 MW; DF3D442BD9C18F80 CRC64;
Query Match 6.7%; Score 8; DB 11; Length 360;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

9 LLLPLML 16
19 LLLPLML 26